

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:40:44 ; Search time 1825.85 Seconds  
(without alignments)  
14750.638 Million cell updates/sec

Title: US-09-889-926-1

Perfect score: 1287  
Sequence: 1 gtcgaccacgctcgtctt.....aaaaaaaaaagggcgccgc 1287

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----	-----	-----	-----	-----	-----

1	1272	98.8	1272	8	AF198054	Arabidops
2	856.4	66.5	96489	8	AC009894	Arabidops
3	856.4	66.5	106320	8	AC002304	Genomic s
4	278.6	21.6	1206	8	AF402602	Phaseolus
5	176.6	13.7	1188	8	AY056327	Arabidops
6	167.2	13.0	81020	8	AB026845	Arabidops
7	162	12.6	1277	8	AB026845	Arabidops
8	157	12.2	1471	8	AF361623	Arabidops
9	156.2	12.1	1307	8	AY062638	Arabidops
10	144.6	11.2	1173	8	PHRNANAM	Arabidops
11	143.4	11.1	1100	8	AF402603	Phaseolus
12	143	11.1	147640	2	AP003542	Arabidops
13	143	11.1	157274	2	AP004679	Oryza sat
14	142	11.0	838	8	AY051015	Arabidops
15	142	11.0	1109	8	AF360201	Arabidops
16	137.4	10.7	961	8	AF404969	Arabidops
17	135.2	10.5	1230	8	AF428375	Arabidops
18	135.2	10.5	1701	8	AY057578	Arabidops
19	134.6	10.5	1202	8	AY045843	Arabidops
20	130.4	10.1	1226	8	AY065268	Arabidops
21	128.2	10.0	138936	2	AF004563	Arabidops
22	125.2	9.7	1216	8	ATAATAF2	Oryza sat
23	125	9.7	954	8	AB049070	Arabidops
24	124.4	9.7	6897	8	AB012243	Arabidops
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26	121.6	9.4	1295	8	STU401151	Solanum t
27	120	9.3	1264	8	AB028183	Oryza sat
28	120	9.3	80376	8	AB010073	Arabidops
29	119.6	9.3	88989	8	AB026658	Arabidops
30	116.8	9.1	81736	8	AB019235	Arabidops
31	115.8	9.0	1090	6	AB2384	Sequence 9
32	115.8	9.0	1090	8	TSP010829	Triticum
33	115.4	9.0	94695	8	ATF23E13	Arabidops
34	115.4	9.0	195452	8	ATCHRIV84	Arabidops
35	115	8.9	18212	8	AP000388	Arabidops
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37	113.8	8.8	1423	8	AB028185	Arabidops
38	113.4	8.8	63654	8	ATAC011698	Oryza sat
39	113.4	8.8	110804	8	ATAC016829	Arabidops
40	113.2	8.8	174264	2	OSJN00003	Arabidops
41	113	8.8	81609	8	AC027035	Oryza sat
42	113	8.8	94487	8	AC012394	Arabidops
43	113	8.8	100806	8	AC015450	Arabidops
44	112.4	8.7	780	8	AY061835	Streptoca
45	112	8.7	2427	8	ART222713	Arabidops

ALIGNMENTS

RESULT	1	AF198054	1272 bp	mRNA	linear	PLN 13-DEC-2000
LOCUS	AF198054	Arabidopsis thaliana	NAC1 (NAC1)	mRNA, complete cds.		
DEFINITION	AF198054	Arabidopsis thaliana	NAC1 (NAC1)	mRNA, complete cds.		
ACCESSION	AF198054	Arabidopsis thaliana	NAC1 (NAC1)	mRNA, complete cds.		
VERSION	AF198054.1	GI:5649235				
KEYWORDS		thale cress.				
SOURCE		Arabidopsis thaliana				
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE		Xie,Q., Frugis,G., Colgan,D. and Chua,N.H.				
AUTHORS		Arabidopsis NAC1 transduces auxin signal downstream of TIR1 to promote lateral root development				
TITLE		Genes Dev. 14 (23), 3024-3036 (2000)				
JOURNAL		20566646				
MEDLINE		2 (bases 1 to 1272)				
REFERENCE		2 (bases 1 to 1272)				
AUTHORS		Xie,Q. and Chua,N.H.				
TITLE		Direct Submission				
JOURNAL		Submitted (24-OCT-1999) plant Cell Biology, Institute of Molecular Agrobiology, 1 Research Link, The National University of Singapore				



TITLE  
JOURNAL

Direct Submission  
Submitted (04-SEP-1999) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

REFERENCE  
AUTHORS

3 (bases 1 to 96489)  
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,  
Altafi, H., Nguyen, M., Lam, B., Buehler, E., Dunn, P., Gonzalez, A.,  
Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luos, S.,  
Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G.,  
Ecker, J., Theologis, A. and Davis, R.W.

TITLE  
JOURNAL

Direct Submission  
Submitted (16-SEP-1999) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

REFERENCE  
AUTHORS

4 (bases 1 to 96489)  
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,  
Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E.,  
Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C.,  
Lenz, C., Li, J., Liu, S., Luos, S., Schwartz, J., Shinn, P.,  
Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and  
Davis, R.W.

TITLE  
JOURNAL

Direct Submission  
Submitted (18-OCT-1999) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

REFERENCE  
AUTHORS

5 (bases 1 to 96489)  
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,  
Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E.,  
Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C.,  
Lenz, C., Li, J., Liu, S., Luos, S., Schwartz, J., Shinn, P.,  
Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and  
Davis, R.W.

TITLE  
JOURNAL

Direct Submission  
Submitted (07-DEC-1999) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

## COMMENT

On Sep 16, 1999 this sequence version replaced gi:5822967.  
'IGF' clone F14J16, gb|AC002304.  
e-mail for correspondence: arab@sequence.stanford.edu  
Genes with similarity to proteins in the databases are described as  
'putative', '-like', or 'similar to'. Genes that have EST  
similarity but no significant protein similarity are described as  
'unknown proteins'. Genes that are annotated based only on gene  
prediction software are described as 'hypothetical proteins'. The  
software programs used to predict genes include: Grail  
(Informatics Group, Oak Ridge National Laboratory,  
<http://compbio.ornl.gov/section/index.html>), GENSCAN (Chris Burge,  
<http://gnomic.stanford.edu/>), Fexa (V.Solovyev & A.Salamov, Sanger Centre,  
<http://genomic.sanger.ac.uk/>), and NetPlantGene (S.M. Hebsgaard, et  
al., CBS, Technical University of  
Denmark, <http://www.cbs.dtu.dk/NetPlantGene.html>).

FEATURES  
source

Location/Qualifiers  
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16877..16948,17113..17184,17313..17384,17854..17925,  
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19631..19829,19908..20066,20165..20283,20388..20598,  
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Query Match	66.5%	Score 856.4	DB 8	Length 96489
Best Local Similarity	90.0%	Pred. No. 1.2e-214		
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QY	286	aaaaatggcatcgtggagaggaagattgatttcacagccaagagacgcaaaaaa	345	
Db	82044	AGNAATGGCATCGCTGGAGGGAGGATTGGTATTTCTACAGCCAAGAGACCGAATA	82103	
QY	346	cgcacgagggtctgagaactaacccagagcaaaogccaccggtatttggaaagccaccggcaa	405	
Db	82104	CGCAGCGGGCTTGAGAACTACCCGAGCAACGGCCACCGGATATTTGGAAGACCGACGGCAA	82163	
QY	406	agacagaaccattcaagaaggtaagctagttgggatgagaagacattggtttctta	465	
Db	82164	AGNACGAACCATTCFPAAGNAGGTAGCTAGTTGGGATGAGGAAGACATTTGGTTTTCTA	82223	
QY	466	tcaagtcgagctctcagggccgtaaaaacgattgggtcatcacgaattccgtctoca	525	
Db	82224	TCAAGGTCGAGCTCCTCGAGGCCGTAAACCGATTGGGTGTCATGCAGGAATTCGGTCTCCA	82283	
QY	526	agatctcatcatctcccaatcattctcgagctctcaaa-----	566	
Db	82284	AGATCTCATCATCTCCCAATCATCTCTGAGCTTCCAAGGTTACACAGTTAAATA	82343	
QY	567	-----	566	
Db	82344	ATCCAGTTATTGATCGTCAGTTAATCTCTCTTAGCAAAATCTTAACGAGTAATATAGT	82403	
QY	567	-----aggaagactgggtcctgtgtagggtattccataagaa	603	
Db	82404	GTTTATGTCTTTGAGGGAAATCAGGAAGACTGGGTCTTGTTAGGGTATTCATTAAGAA	82463	
QY	604	tacggaagaggttatatgagagacaacatgggaagcgtttgtatgagacagcctctgc	663	
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QY	664	atcgcttctccactgatggatccttatcaactttgacaaagaccctctttatct	723	
Db	82524	ATCGCTTCCTCCACATGATGGATPCTTCATCAACTTTGACCAAGAACCCCTCTTCTATCT	82583	
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Db	82704	GAAACCCCTAACCCCTTGTTTACTGCTGGTTCAGCCCTCAGCCACGCTCAGGCTTCGACTC	82763
Qy	904	attcgtcttcacatcagatgggttcacagctctactcagctcagctcagctcagctcagctcagctc	963
Db	82764	ATTCTGTTCTTCAGATCAGATGGTTCACAGAGCTCTACTCAGTCAGCTCAGTAAAGATTGA	82823
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Qy	1204	cacttatgacctagacatacatatattcctcagctagctcagctcagctcagctcagctcagctc	1263
Db	83064	CACATTACGCTAGACATACATATTTTCATCTGATGTTTCCATTTGTTTCAAGCTATTA	83123
RESULT	3		
AC002304/c			
LOCUS	AC002304	106320 bp	DNA linear
DEFINITION	Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome 1, complete sequence.		
ACCESSION	AC002304		
VERSION	AC002304.3	GI:7798719	
KEYWORDS	HTG.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	1 (bases 1 to 106320) Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altati, H., Bei, Q., Chin, C., Chlou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howling, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federpsiel, N.A., Theologis, A. and Ecker, J.R.		
TITLE	Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome 1		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 106320) Ecker, J.R.		
AUTHORS	Direct Submission		
TITLE	Submitted (21-JUN-1997) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA		
JOURNAL	3 (bases 1 to 106320) Ecker, J.R.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (20-AUG-1997) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA		
JOURNAL	4 (bases 1 to 106320) Ecker, J.R.		
REFERENCE			
AUTHORS			



**TITLE**  
**JOURNAL**  
Direct Submission  
Submitted (14-APR-2000) Arabidopsis thaliana Genome Center,  
Department of Biology, University of Pennsylvania, 38th Street and  
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
**REFERENCE**  
**AUTHORS**  
5 (bases 1 to 106320)  
Ecker, J.R.  
**TITLE**  
**JOURNAL**  
Direct Submission  
Submitted (13-MAY-2000) Arabidopsis thaliana Genome Center,  
Department of Biology, University of Pennsylvania, 38th Street and  
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
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Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,  
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Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,  
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Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.  
**TITLE**  
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Direct Submission  
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Hamilton Walk, Philadelphia, PA 19104-6018, USA  
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AB026645

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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Clone:MGH6.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (sites)

Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones

DNA research : an international journal for rapid publication of reports on genes and genomes. 7 (2), 131-135 (2000)

20277480

2 (bases 1 to 81020)

Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S. Direct Submission

Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see <http://www.kazusa.or.jp/kaos/cgi-bin/agd.graph.cgi?c=MGH6>

Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Grail-1.3/>), GENSCAN (Chris Burge, MIT, <http://CGB-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://grmlini.zool.iastate.edu/cgi-bin/sp.cgi>).

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MJM20 and the 3' clone is MJG19.





## ORIGIN

Query Match 12.2%; Score 157; DB 8; Length 1471;  
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 Matches 298; Conservative 0; Mismatches 170; Indels 9; Gaps 3;

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QY 190 cgattactatgagacgattcgtcttcaataatcgtaccaccctcttctctatcca 249  
 Db 313 AACTCACTACTCAAGAGAGAGGTCTTCAACATCCGATTACCGCGCAGCGATTGGTCA 372

QY 250 agtcgattcaacaagtgtagcttgagacatcccaaaaatgcatgctgggagggaa 309  
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 Db 433 GGAGTTTACTTTTCTGCGAGAGGATCGGAAGTATCCGACCGGATGAGGACCG 492

QY 370 agcaacggccacggatattggaagaccacggcgaagaca---gaaccattctaa 426  
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QY 487 cctgaacacggattggtgctcacgaattccgtctcccaaggtatcctatcctcccaa 546  
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QY 547 tcattctcagctctccaaaggaagactgggtctgtgtagggattccataagaa 603  
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 DEFINITION Arabidopsis thaliana Unknown protein (MR12.1) mRNA, complete cds.  
 ACCESSION AY062638  
 VERSION AY062638.1 GI:17065123  
 KEYWORDS FLI-CDNA.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 1307)  
 Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, H., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Hayashizaki, K., Ecker, J., Theologis, A. and Davis, R.W.  
 Direct Submission  
 Submitted (14-NOV-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA  
 e-mail for correspondence: arab@sequence.stanford.edu

## COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : "RIKEN Arabidopsis Full-length cDNA") : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M.,

Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

## FEATURES

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BASE COUNT 422 a 222 c 262 g 401 t

## ORIGIN

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QY 122 ataagcattggtggaggcaaaagtctcccggttcagattccaccgaaggacgagtag 181  
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QY 182 cttgtctgcattactctgagacgacgctctcacaataatcatcaccacacctctgtc 241  
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QY 242 ctgattccaaagtcgattctcaacaagtgtgagccttggagacatcccaaaaatggcatcg 301  
 Db 293 ATTGCTGAAGTTGATCTCAACAAAGTCGACCTTGGGACITGGCTTGGGAAGGCTAAGCTT 352

QY 302 ggagggaagattggttattctacagcccaagagacgcaaaaatcacgcagcgggctgaga 361  
 Db 353 GGGCAAAAAGAGTGGTACTTCTTTGGTGAAGAGACCGGAAATACCCGACTGTTTAAGA 412

QY 362 actaacgagcaacgcccacggatattgaaagccacggcgaagacagaaacattctta 421  
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QY 422 agaaagggaagctagttggatgaggaagacattggtttctctcaaggtcagctcct 481  
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QY 482 cgaggcgtaaaacgattgggtcagcgaattccgtctccaaggtatctcatcact 541  
 Db 533 AAAGGAGTAAACAAATTTGGTTCATGATGATGATGATGATGATGATGATGATGATGAT 592

QY 542 cccaatcatctctgagctctccaaaggaagacgtgggtcttctgtgtaggtattccaaag 601  
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Db	89	TCGCCCTGGCTTTAGGTTTTCACCAACGAGGAGGAACAAATCGTCTACTACCTTTGCA 148
Qy	204	gacatgccttcaataatcatgacacacctctgttcctgatcccaagtcatcaaca 263
Db	149	ACCAAGC---CACATCAAAAGCTTTGCCCTGCTCCATCATCCAGAAAGTGGATCTTACA 205
Qy	264	agtgagccttgaggacatcccaaaatgagcgtgaggaggaagattggtattct 323
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Qy	324	acagccaaagagacccgaataacagcagcggggctgagaactaacccagagccacccg 383
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Qy	384	gatattgaaagccaccgcaagacagaaacattcttaagaaaagggttaagctagtggga 443
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Qy	504	tcattgacgaattcgtctccaaagatctcatatcc---tcccaatcattctctgagct 560
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ACCESSION	AP003542	
VERSION	AP003542.1 GI:13810548	
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SOURCE	Oryza sativa (cultivar:Nipponbare) DNA, clone:P0589C03.	
ORGANISM	Oryza sativa	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.	
AUTHORS	1 (sites)	
TITLE	Sasaki,T., Matsumoto,T. and Yamamoto,K.	
JOURNAL	Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0589C03	
REFERENCE	Published Only in DataBase (2001) In press	
AUTHORS	2 (bases 1 to 147640)	
TITLE	Sasaki,T., Matsumoto,T. and Yamamoto,K.	
JOURNAL	Submitted (25-APR-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan	
COMMENT	(E-mail:tsasaki@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)	
	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.	
	* NOTE: This is a 'working draft' sequence.	
	* This sequence will be replaced	
	* by the finished sequence as soon as it is available and	
	* the accession number will be preserved.	
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Db	55582	GCTGGACGCGAGCTGCCCGGGGTTCCGGTTCCACCGGAGGAGCTGATCAC 55523
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Db	55522	CTACTACTGCTCGGAAGTGTGGACGGGAGCTTCAACG---GGCGGCCCATCGCGGA 55466
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Qy	310	ggattggtatttctacagccaaagagacgaaaaatacgcgacgggctgagaactaacg 369
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VERSION	AP004679.1 GI:18447938	
KEYWORDS	HTG; HTGS, PHASE2	
SOURCE	Oryza sativa (cultivar:Nipponbare) DNA, clone:OSJNBa0021N09.	
ORGANISM	Oryza sativa	
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AUTHORS	1 (bases 1 to 157274)	
TITLE	Sasaki,T., Matsumoto,T. and Yamamoto,K.	
JOURNAL	Submitted (30-JAN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan	
COMMENT	(E-mail:tsasaki@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)	
	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.	
	* NOTE: This is a 'working draft' sequence.	
	* This sequence will be replaced	
	* by the finished sequence as soon as it is available and	
	* the accession number will be preserved.	

\* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

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RESULT 14
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DEFINITION cds.
ACCESSION AY051015
VERSION AY051015.1 GI:15293162
KEYWORDS F10D13_14
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    Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 838)
AUTHORS Yamada,K., Liu,S.X., Pham,P.K., Banno,F., Onodera,C.S., Quach,H.L.,
    Goldsmith,A.D., Jiang,P.X., Lee,J.M., Tanaka,M., Onodera,C.S., Quach,H.L.,
    Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
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    Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and
    Theologis,A.
    Full Length cDNA of gene F10D13_14 (GI:12597796)
    Unpublished
REFERENCE 2 (bases 1 to 838)
AUTHORS Yamada,K., Liu,S.X., Pham,P.K., Banno,F., Onodera,C.S., Quach,H.L.,
    Goldsmith,A.D., Jiang,P.X., Lee,J.M., Tanaka,M., Onodera,C.S., Quach,H.L.,
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    Theologis,A.

```

Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L.,  
 Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L.,  
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
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 Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,  
 Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and  
 Theologis,A.  
 Direct Submission  
 Submitted (01-AUG-2001) Plant Gene Expression Center, 800 Buchanan  
 Street, Albany, CA 94710, USA  
 The RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
 Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,  
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGENC (SSP) Consortium members constructed and  
 sequenced the PUN1 (ORF) clones using the RAFL cDNAs: Yamada,K.,  
 Liu,S.X., Pham,P.K., Banno,F., Dale,J.M., Goldsmith,A.D.,  
 Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,  
 Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H.,  
 Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B.,  
 Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,  
 Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGENC) and Seki, M. (RIKEN GSC) contributed equally  
 to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP  
 /PGENC) contributed equally to this work as PIs.

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Db 143 AATTCGACCCATGCAATACCCGAGAAACACAGAGTTTGGAGAAATACAGTGGTATTCT 202
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:40:44 ; Search time 1596.85 seconds

(without alignments)  
10878.029 Million cell updates/sec

Title: US-09-889-926-1

Perfect score: 1287

Sequence: 1 gtcaccacgctcgtctt.....aaaaaaaaagggcgccgc 1287

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthma:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	615.8	47.8	1132	12	B08241	B08241 F23117-Sp6.
2	606.4	47.1	608	9	AV540514	AV540514 AV540514.
3	540.4	42.0	1142	12	B08263	B08263 F27J24-Sp6.
4	482	37.5	482	9	AV536694	AV536694 AV536694
5	351	27.3	351	9	AV538912	AV538912 AV538912
6	337.6	26.2	1026	12	B10411	B10411 F23117-Sp6
7	312	24.2	1069	12	B11695	B11695 F27J24-Sp6
8	252.6	19.6	739	10	BM112823	BM112823 EST560359
9	229.6	17.8	494	10	BM123181	BM123181 I018P63P
10	225.2	17.5	640	10	BE555459	BE555459 sp89f05.Y
11	217.4	16.9	715	10	BM112826	BM112826 EST560362
12	213.4	16.6	467	10	BM112890	BM112890 I014P44P
13	212.2	16.5	598	10	BG791220	BG791220 EST560362
14	208.6	16.2	505	9	AW234514	AW234514 sfl5b08.Y
15	208	16.2	441	10	BE554923	BE554923 sp8ze11.Y
16	204.6	15.9	418	10	BM123635	BM123635 I026P45P
17	204	15.9	466	9	AW685143	AW685143 NF026A09N

18	201.6	15.7	401	10	BI125742	BI125742 I065P37P
19	198.8	15.4	564	10	BF650098	BF650098 NF087H02E
20	197.6	15.4	445	9	AW032569	AW032569 EST276128
21	183.2	14.2	721	10	BE586058	BE586058 Est#8pt7_
22	169.4	13.2	410	9	AW203239	AW203239 s27f12.Y
23	168.4	13.1	594	12	B25594	B25594 F28E15TR IG
24	166.8	13.0	757	10	BG587963	BG587963 EST489738
25	165.8	12.9	700	10	BF635413	BF635413 NF077C03D
26	165.8	12.9	795	12	BH542565	BH542565 B0HP656TF
27	165.2	12.8	843	10	BI308121	BI308121 EST529531
28	161.8	12.6	772	10	BE661301	BE661301 588 GmaxS
29	158.2	12.3	566	10	BE594436	BE594436 P11_33_D0
30	157	12.2	675	10	BG452685	BG452685 NF078C02L
31	155.4	12.1	638	9	AV923588	AV923588 AV923588
32	155.2	12.1	477	9	AV928528	AV928528 AV928528
33	148.6	11.5	383	9	AA660001	AA660001 EST00051
34	148.2	11.5	405	10	BG510816	BG510816 sac73f07.
35	147	11.4	625	9	AW185617	AW185617 se80b05.Y
36	143.6	11.2	313	9	AI965921	AI965921 sc79g06.Y
37	142.8	11.1	562	9	AV836291	AV836291 AV836291
38	142	11.0	660	10	BG448728	BG448728 NF045C09N
39	142	11.0	726	10	BG647072	BG647072 EST508691
40	140.8	10.9	631	9	AW329169	AW329169 N200380e
41	140.4	10.9	434	10	BE596175	BE596175 P11_50_E0
42	140.4	10.9	529	10	BE804888	BE804888 ss34d06.Y
43	140.4	10.9	613	10	BF644336	BF644336 NF063H08E
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45	139.4	10.8	373	10	BE555014	BE555014 sp83f08.Y

#### ALIGNMENTS

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LOCUS B08241 1132 bp DNA linear GSS 14-MAY-1997  
DEFINITION F23117-Sp6.1 IGF Arabidopsis thaliana genomic clone F23117, DNA  
ACCESSION B08241  
VERSION B08241.1 GI:20893363  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 1132)  
AUTHORS Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and  
Ecker, J.  
TITLE BAC End Sequences at ATGC  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSs: F23117-T7.1, F23117-T7, F23117-Sp6  
Contact: Ecker J.  
Arabidopsis Thaliana Genome Center  
University of Pennsylvania  
Dept. of Biology, University of Pennsylvania, Philadelphia, PA  
19104  
Tel: 215-898-9384  
Fax: 215-898-8780  
Email: jecker@atgenome.bio.upenn.edu  
Seq primer: Sp6  
Class: BAC ends  
High quality sequence start: 93  
High quality sequence stop: 846.  
Location/Qualifiers  
1..1132  
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/strain="Columbia"  
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/clone="F23117"  
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/note="Vector: BeloBACII; Site\_1: EcoRI; Site\_2: EcoRI;

BASE COUNT 324 a 272 c 207 g 322 t 7 others  
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Produced by Thomas Altmann"  
 Query Match 47.8%; Score 615.8; DB 12; Length 1132;  
 Best Local Similarity 92.4%; Pred. No. 8.1e-100;  
 Matches 658; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

QY 567 aggaagactgggtcttggtaggtattccataagaatcaggaagaggttatattatagag 626  
 Db 269 AGGAAGACTGGGTCTGTGTAGAGGTATCCATAAGAAACGGAAGAGGTATATGTAGAG 328  
 QY 627 acaaatgggaagctgttttggtagagagcctctgcctgccttccctccactgatgac 686  
 Db 329 ACAACATGGGAAGCTGTTTGTAGAGAGCCCTCTGCATCGCTTCTCCACTGATGGATC 388  
 QY 687 cttacataacatttgacaaagacctcttcttctcagtgatgatcatcatcatca 746  
 Db 389 CTTCATCAACCTTGAACCAAGAACCCCTCTTCTATCTCAGTGATGATCATCATCATCA 448  
 QY 747 tcaatgagcagctacccctcttctccaatgttcacagaaaccccttaaacctgaacc 806  
 Db 449 TCNATGAGCAGCTACCCCTCTCTCTCAATTTGTACAGAACCAACCTTAACTCGAACC 508  
 QY 807 taaccaactcagctctctgaactcaagattccatgcaagaacccctaacccctgtttact 866  
 Db 509 TAACCAACTCAGTCTCTGAACCTCAAGATTCCATGCCAAGAACCCCTAACCCCTGTTTACTG 568  
 QY 867 ggtgttcagcctcagccagctcagagcctcagctcagctcagctcagctcagctcagct 926  
 Db 569 GTGGTTTCAGCCCTCAGCCAGCCCTCAGAGCCCTCAGCTCATCTCTGTTCTCAGATGAGTGG 628  
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 QY 987 cacagagttatggagaagtagctcggagagcctcctcagcagacatcggtattccaagca 1046  
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 QY 1047 ctgttgggaattgctgatcagctgagtaacgagaggttactattgtcttatctcctacca 1106  
 Db 749 CTGTTGGGAATTCGCTGATGATCGAGTGTACGAGAGTACTAATGCTATATTCCTATCCA 808  
 QY 1107 tgattgaaacattcttcgggggaaataacgctgtgctgtgtgtattgtacaaacatttc 1166  
 Db 809 TGATTGGAACATTCCTCGGGGGGAAATAAACCCTGCTGTCTGAATGTTCAACATTCCTCC 868  
 QY 1167 ctcaactcttgacacagctagatcatgtaaaataacacattatgacgtgagacatacat 1226  
 Db 869 CTCACCTCGGTTCGCCGCTGAAATTCAGTAAATAACCACTAATAACCCCTAAACCTCCCT 928  
 QY 1227 ata-tttcctcgtagttccattgtttccaaaaaaataaaaaaaataaaaaa 1277  
 Db 929 TTAATTTTCCCGGTATTCCTCCATTTGTTTCAAGGTATTAAGGGACCTTAAACA 980

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 AV540514  
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 DEFINITION AV540514 Arabidopsis thaliana roots Columbia linear EST 06-SEP-2000  
 CDNA clone RZ151B06F 3', mRNA sequence.  
 AV540514  
 ACCESSION AV540514.1 GI:8702272  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 608)  
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries  
 DNA Res. 7, 175-180 (2000)  
 20363093  
 Contact: Erika Asamizu  
 The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
 Email: asamizukazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
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Query Match 47.1%; Score 606.4; DB 9; Length 608;  
 Best Local Similarity 99.8%; Pred. No. 4.7e-98;  
 Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 ttatctcttctcttaacatccactcaatacaaacactaaacactagaataaaaaag 79  
 Db 1 TTATCTCTCTTCTCTTAACCATCCACTAATCATACATAAACCCTAGAAAAAAG 60  
 QY 80 gatcaatcatgtgagcgggaagagatgaagaaagttagtataagcatggtgaggaca 139  
 Db 61 GATCAATCATGTGAGACGGGAAGAGATGAAGAAAGTAGTAGTAAGCATGTGTGAGGCA 120  
 QY 140 aagttgctcctcgggttcagatttcacccgaagagatgagcttctcgcgattacttg 199  
 Db 121 AAGTTGCTCTCGGATTCAGATTTCACCCGAGACGATGAGCTTGTCTCGGATTTACTTG 180  
 QY 200 atgagagcgtcgtctcaataatcatcgaccacctctgtcctgatcccaagtcgactc 259  
 Db 181 ATGAGACGATCGCTTCAATAATCATCGACCACTCTTGTCTGATCCAAAGTCGATCTC 240  
 QY 260 acaagtgtagccttgaggacatcccaaaaatggcagctggtggagggaaggttgat 319  
 Db 241 AACAAAGTGTGAGCTTGGGACATCCCAAAAATGGCATGCGTGGGAGGAAGGATTTGAT 300  
 QY 320 ttctacagcacaagagaccgaaataacgcagcgggctgagaactaacccagcaacggcc 379  
 Db 301 TTCTACAGCCAAAGAGACCCGAAATAACCCGCGGCTGAGAACTAACCGAGCAACGGCC 360  
 QY 380 accggtattggaaagccaccggcacaagacagaaacattcttaagaagggttaagctagt 439  
 Db 361 ACCGGATATTGGAAGCCACCAGCAAGACAGAACCACTTCTAAGAAAGGGTAAGCTAGTT 420  
 QY 440 gggatgaggagacattggttttctatcaagggtcgagctcctcgagccgttaaacccgat 499  
 Db 421 GGGATGAGGAAGACATTTGGTTTCTATCAAGGTGAGCTCCTCGAGGCCGTAAACCCGAT 480  
 QY 500 tgggtcatgcacgaattccgtctcgaaggatctcatcatctcccaatctctctgagc 559  
 Db 481 TGGGTGATGACGAAATTCCTGCTCAAGGATCTCATCATCTCTCCCAATCATTTCTGAGC 540  
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 Db 541 TCTCCAAAGGAAGACTGGGTCTTGTGTAGGTATTCCATAAGAAATACGGAAGGTATATA 600  
 QY 620 tgtagaga 627  
 Db 601 TGTAGAGA 608

## RESULT 3

B08263  
 LOCUS B08263.1 1142 bp DNA linear GSS 14-MAY-1997  
 DEFINITION F27J24-Sp6.1 IGF Arabidopsis thaliana genomic clone F27J24, DNA sequence.  
 ACCESSION B08263  
 VERSION B08263.1 GI:2089385  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 1142)  
 AUTHORS Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.  
 TITLE BAC End Sequences at ATGC  
 JOURNAL Unpublished (1997)  
 COMMENT Other\_GSSs: F27J24-T7, F27J24-Sp6  
 Contact: Ecker J.  
 Arabidopsis Thaliana Genome Center  
 University of Pennsylvania  
 Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104  
 Tel: 215-898-9384  
 Fax: 215-898-8780  
 Email: jecker@atgenome.bio.upenn.edu  
 Seq primer: Sp6  
 Class: BAC ends  
 High quality sequence start: 87  
 High quality sequence stop: 816.  
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 /clone="F27J24"  
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 Produced by Thomas Altmann"

## FEATURES

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 Best Local Similarity 90.3%; Pred. No. 1.9e-86;  
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 Db 263 AGGAGACTGGGTCTGTGTAGGGTATTCATAAGAAATACGGAAGGTTATGTAGAG 322  
 QY 627 aaacatggaagctgtttgtatgagacagcctctgcacgtcttctccactgatgac 686  
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 QY 687 ctatcatcaacttgaccagaacccctcttcttctcagtgatgatcatcatcatca 746  
 Db 383 CTTACATCAACTTTGACCAAGAACCTCTTCTATCTCAGTGATGATCATCATCATCA 442  
 QY 747 tcaatgagcacgtaccctgcttctccaatttgtcacagaaaccccttaactgaacc 806  
 Db 443 TCAATGAGCACGTACCCCTCTTCTCCAAATTTGTACAGAACCAACCTTAAACTCGAAC 502  
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 Db 503 TAACCAACTCAGTCTCTGAACCTCAGATTCAGATTCCTATGCAAGAACCTTAACCCCTGTATTAGT 562  
 QY 867 gtggttcagctccagccagctcacaggcctcagctcattctgttcttcagatcagatgg 926  
 Db 563 GTGGTTCAGCCTCAGCCAGGCTCACAGGCTCGACTCATCTGTCTTCAGATCATGATGG 622

QY 927 ttctcagagctctactcagctcagctcactaagattggaagctcgggcctaagaat 986  
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 QY 987 cacagagttatggagaagtgtagctcgagagcctctgacccgacatcggtattccagca 1046  
 Db 682 CACAGAGTTATGGAGAAAGGTACTCGGATAGCTTCTCTGACCGACATCGTATCCACCA 741  
 QY 1047 ctggttggaattgctgagtcgagtgtaacgagagttactatgctatatctctatoca 1106  
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 QY 1107 tgattggacaattcttcggggggaataacgtgtgctgtctgctgctgatacaaacattc 1166  
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 Db 919 CTTATTTTCAACGTAATTCCTATTTGTTCCAGGGTTATTAAGGACCTCTATAAAA 972

## RESULT 4

AV536694  
 LOCUS AV536694 482 bp mRNA linear EST 06-SEP-2000  
 DEFINITION AV536694 Arabidopsis thaliana liquid-cultured seedlings Columbia  
 Arabidopsis thaliana cDNA clone PAZNI10438R 5', mRNA sequence.  
 ACCESSION AV536694  
 VERSION AV536694.1 GI:8696977  
 KEYWORDS EST.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 482)  
 AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
 TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries  
 JOURNAL DNA Res. 7, 175-180 (2000)  
 MEDLINE 20363093  
 COMMENT Contact: Erika Asamizu  
 The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
 Location/Qualifiers  
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 /strain="Columbia"  
 /db\_xref="taxon:3702"  
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 /clone\_lib="Arabidopsis thaliana liquid-cultured seedlings  
 Columbia"  
 /tissue\_type="liquid-cultured seedlings"  
 /note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: Xhoi"

BASE COUNT 160 a 104 c 123 g 95 t  
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 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 33 cctcttaaccatcactaatcaaacactaaacctagaaaaaaggatcaaatcagg 92  
 Db 1 CCTCTTAACCATCCACTAATCAACACTAGAAAAAAGGATCAATCATG 60







Utterback, T., Chiemiango, A., Bougri, C., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.  
 Generation of ESTs from potato roots  
 Unpublished (2001)  
 Contact: Research Genetics, Libraries Division  
 Tel: 1-800-711-6195  
 Email: cdna@resgen.com  
 For clone info: please contact Research Genetics, Libraries Division  
 Division tel 1-800-711-6195, email cdna@resgen.com  
 Seq primer: T3.

FEATURES  
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 BASE COUNT 251 a 160 c 135 g 193 t  
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 Best Local Similarity 64.7%; Pred. No. 2.3e-35;  
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 QY 100 aqaagagatgaagaaagtagtataagcatggtgaggaagaaagttgctcgcggtacag 159  
 DB 16 AANAATGATACACACAGCAGCTTGAGCATGGTGGAAATCCAAATACACACAGGATTAG 75  
 QY 160 attcaccgaaggacgatgagctgtgtcgattacttgatgacgatcgcttca--- 216  
 DB 76 ATTTCATCCAGATGAAGAAGTATTGTGATCTACTTAATGAAGAAGTTGATCAATC 135  
 QY 217 caataatcatcgacacaccttctgctgatccaagtcatgatacgaagtgatgagccttg 276  
 DB 136 CACAGACCAACCAATAACCTCTTCTCATAGAAGTTGACCTCAATAAATCCGAACCTTG 195  
 QY 277 ggacatcccaaaaatggcatcgctggggaaggaagattggtattctacagccaaagaga 336  
 DB 196 GGAATTCCTGAAGTGGCATGTTGGAGGCAAGGATGGTACTTCTACACCCCAACGTGA 255  
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 DB 256 CGAAAATACGCGAGCGGGCTCCGAACAAACAGAGCCACCGTATCTGTTACTGGAAAGC 315  
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 DB 436 CGCCCTTGATGAAGGTCCCTCTAGTAACATTCGTTCTCAAAATTTCTCTCAAGGAGGA 495  
 QY 574 ctgggtcttgtagggtatctccataagaatacaggaagagatt-----at 618  
 DB 496 TTGGGTATTATCCCGAGTATTTCACAAAGCAAGGAATTTACTTCTCTCAAGCAAGAA 555  
 QY 619 atgtagacacacatgggaaggtgtttgtgagacagcctctcgtcctccact 678  
 DB 556 TGGANGCAACACATATACTACGATAACGATACATAAGTCTTCTCAATC-TTTACACCAT 614

QY 679 gatggtccttacatcaacttggaccaagaacctcttcttcttctcagtgatgataca 738  
 DB 615 AATGGATCCTTACATTACTTTCGACCAATAAATAC---CCTAACCAATATCCATATGAA 671  
 QY 739 ctacatcatcaatgagcagctaccctgtctctcaattgtgtcacagaacaaacctaa 797  
 DB 672 TGAATTATATATGAGCGAGTCCCTGCTTCTCTCATTTTCCACCCCTAACCAACTTTCA 730  
 RESULT 9  
 BI123181  
 LOCUS 494 bp mRNA linear EST 31-DEC-2001  
 DEFINITION 1018P65P Populus leaf cDNA library Populus tremula x Populus tremuloides cDNA, mRNA sequence.  
 ACCESSION BI123181  
 VERSION BI123181.1 GI:18007156  
 KEYWORDS EST.  
 SOURCE Populus tremula x Populus tremuloides.  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.  
 REFERENCE 1 (bases 1 to 494)  
 AUTHORS Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlert, R., Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and Lundberg, J.  
 TITLE Gene expression in Populus  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Erlandsson R  
 Department of Biotechnology  
 Royal Institute of Technology  
 Teknikringen 30, Stockholm S-10044, Sweden  
 Tel: 46 8 790 8287  
 Fax: 46 8 245452  
 Email: rikerlebiochem.kth.se.  
 FEATURES  
 source  
 1..494  
 /organism="Populus tremula x Populus tremuloides"  
 /db\_xref="taxon:47664"  
 /clone.lib="Populus leaf cDNA library"  
 /note="Organ: leaf"  
 BASE COUNT 147 a 102 c 128 g 117 t  
 ORIGIN

Query Match 17.8%; Score 229.6; DB 10; Length 494;  
 Best Local Similarity 73.3%; Pred. No. 3.1e-31;  
 Matches 311; Conservative 0; Mismatches 104; Indels 9; Gaps 1;  
 QY 105 agatgaagaaagtagtataagcatggtgaggaagaaagttgctcgcggtacagatttc 164  
 DB 61 AGAGAAAGATGACACATTAAGCTTCGTGGAGGCAAACTGCCACCGGTTAGGTTC 120  
 QY 165 acccggaaggacgatgagctgtgtcgattacttgatgagacgatcgtctcaataatc 224  
 DB 121 ATCCAAGATGAAGAGCTTGTATGTGATTCTGTATGA-----AGAAGGCTTCTC 171  
 QY 225 atcgaccacctgtctcgatccaagtcatcacaagtgtgagccttggaacatcc 284  
 DB 172 ACTGCGACTCCCTTCATGATAGAGGTGACCTCAACAGTGTGAGCCTTGGGATTTTC 231  
 QY 285 caaaaaaggcgtcggtggaggaagattggtatttctacagccaaagagaccgaaat 344  
 DB 232 CTGAACCGCATCGGTGGAGGCAAGGAATGGTACTTTTACGCCAAACAGATCGTAAT 291  
 QY 345 acgcgcaggggctgagaactaacccagcagccagcccggtatttgaaagccacggca 404  
 DB 292 ATGCAACTGGACTAAGAAGCTTAATCGAGCAACAGCATCTGGATATTGGAAGGCCGGA 351  
 QY 405 aagacagaaccattctaaagaaaggttaagctagttggatgaggaacatgtgtttct 464

Db 352 AGGACACATATCTACGTAAAGGACACCTTGTGGCATGAGAAAGACCTTGGTGTGCT 411  
 Qy 465 atcaagtcgagctctcctcggcgccgtaaaacccgattgggtcgcacgaattcgtctcc 524  
 Db 412 ACCAAGGTAGGACCTTAAGGAAACCAACCGATTGGGTAATGCATGAGTTTCGCGCTTG 471  
 Qy 525 aagg 528  
 Db 472 AAGG 475

RESULT 10  
 BE555459  
 LOCUS  
 DEFINITION  
 SP89F05.y1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-cl045-826 5' similar to TR:Q40880 Q40880 NAM GENE. [1] ;, MRNA  
 sequence.  
 ACCESSION  
 VERSION  
 BE555459  
 BE555459.1 GI:9819946  
 EST.  
 SOURCE  
 soybean.  
 ORGANISM  
 Glycine max

REFERENCE  
 AUTHORS  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna  
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers  
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk  
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann  
 R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: Resgen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntville, AL 35801 For further information  
 call: (800)-533-4363 or contact via email: ccu@resgen.com  
 Insert length: 1555 Std Error: 0.00  
 High quality sequence stop: 427.

FEATURES  
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 1. 640  
 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl045-826"  
 /clone\_lib="Gm-cl045"  
 /tissue\_type="Hypocotyl, 9-10 day old etiolated seedlings"  
 /lab\_host="DH10B"  
 /note="vector: pBluescriptII SK+; Site 1: EcoRI; Site 2:  
 XhoI; This cDNA library was constructed from mRNA isolated  
 from etiolated hypocotyl tissue of 9-10 day old seedlings  
 of the cultivar Williams 82. Complementary DNA was  
 synthesized from mRNA using a primer consisting of a  
 poly(dT) primer with a XhoI restriction site. EcoRI  
 adapters were ligated to the blunt-ended cDNA fragments  
 followed by digestion with EcoRI and XhoI. The cDNA  
 fragments were directionally cloned into the EcoRI-XhoI  
 restriction site of the pBluescript vector. The ligated  
 cDNA fragments were transformed into DH10B host cells  
 (Gibco BRL). This library was constructed by Dr. Randy  
 Shoemaker."

BASE COUNT  
 ORIGIN  
 175 a 138 c 150 g 173 t 4 others

Query Match 17.5%; Score 225.2; DB 10; Length 640;

Best Local Similarity 71.2%; Pred. No. 1.7e-30;  
 Matches 312; Conservative 0; Mismatches 117; Indels 9; Gaps 1;

Qy 116 agtagtataagcatcgttgagagcaaaagtgtcctcgggattcagattttcaccacccaagagac 175  
 Db 111 AGCAACATAGCATGGTAGAGGCAAGCTGCCACAGGATTCAGGTTTTCATCCAAGAGAT 170  
 Qy 176 gatgagcttctcgtattacttgatgagacgatcgttcacaataatcgcaccacct 235  
 Db 171 GAAGAGCTTGTGTGATTACTTGTATGAAGAAGGTGCAACACATGAT-----TCC 221  
 Qy 236 attgtcctgattcccaagtcgatctcaacaagtgtgagccttggtgacatcccaaaaaatgga 295  
 Db 222 CTTCTCTTATAGATGTTGACCTTAACAAGTGTGAGCCATGGGATATTCTCTGAACACGA 281  
 Qy 296 tgcgtggaggaagattggtattttcacagccaaaagagaccgaaataacgcagcgggg 355  
 Db 282 TGCCTTGGAGGGAAGAGTGGTATTTCTACACAAAGAGACCCGTAAGTATGCAACAGG 341  
 Qy 356 ctgagaactaacccgagcaacggccaccgataattggaagccaccggcgaagacagaacc 415  
 Db 342 TTACGCACAAATCGTGCCTACTGCCTCAGGGTATTGGAAGGCCACAGGAGGACAGGCT 401  
 Qy 416 attctaagaaaagggtaagctagttgggtgaggaagacattggttttctatcaagttgca 475  
 Db 402 ATCCTCCGCAAGGCCACCCATGATAGGGATGGAGAAGACNTTGGTGTCTTATCAAGGAAG 461  
 Qy 476 gctctcggagcgcgttaaaacccgattgggtcgtacgcgaattcctcgaaggtctcat 535  
 Db 462 GCACNCANAGGAGGAANAACATGGATGGGTCATGTCATAGTTTCGATCGAAGGACCTGAT 521  
 Qy 536 catctctcccaatcattct 553  
 Db 522 GGACCTCCTTAAATTTCT 539

RESULT 11  
 BM112826  
 LOCUS  
 DEFINITION  
 EST560362 potato roots Solanum tuberosum cDNA clone cPRO16A15 5',  
 end, mRNA sequence.  
 ACCESSION  
 VERSION  
 BM112826.1 GI:17073874  
 EST.  
 KEYWORDS  
 SOURCE  
 potato.  
 ORGANISM  
 Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 715)  
 van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,  
 Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,  
 Tanksley, S. and Baker, B.  
 Generation of ESTs from potato roots  
 Unpublished (2001)  
 Contact: Research Genetics, Libraries Division  
 Tel: 1-800-711-6195  
 Email: cdna@resgen.com  
 For clone info: please contact Research Genetics, Libraries  
 Division tel 1-800-711-6195, email cdna@resgen.com  
 Seq primer: T3.

FEATURES  
 Location/Qualifiers  
 source  
 1. 715  
 /organism="Solanum tuberosum"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="cPRO16A15"  
 /clone\_lib="potato roots"  
 /tissue\_type="roots"  
 /dev\_stage="in vitro grown stem cuttings"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; supplier: Cornell University, Tanksley lab;

sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

BASE COUNT 242 a 153 c 134 g 186 t  
ORIGIN

Query Match 16.9%; Score 217.4; DB 10; Length 715;  
Best Local Similarity 67.3%; Pred. No. 4e-29;  
Matches 368; Conservative 0; Mismatches 171; Indels 8; Gaps 4;

Qy 100 agaagagatgaagaagtagtataagcattggtggagcaagtgcctccgggattcag 159  
Db 16 AAAAAATGAGTAACACAGCAGCTTCAGCATGGTGAATCCAAATTACCACAGGATTTAG 75

Qy 160 attcaccgaagacacatagctgtcgtgattctatgtatgagacgattcgttca--- 216  
Db 76 ATTTCATCCAGAGATGAAGAACCTTATTGTGATTACTTAATGAAGAAAGTTGATCAATC 135

Qy 217 caataatcatgaccacacctcttctcctgattcccaagtgcattcaacaagtgtgagccttg 276  
Db 136 CACAGACCAACAACAATACCTCTCTCATAGAAGTTGACCTCAATAAATCCGAACCTTG 195

Qy 277 ggacatccccaaaaatggcattgctgggaggaaggattggtatttctacagcccaagaga 336  
Db 196 GGAATATCTCGAAGTGCATGTGTTGGAGCAAGGATTGTTACTTCTACAGCCCAAGCTGA 255

Qy 337 ccgaaatacgcagcggcgtgaaactaacagcaacgcccacggatattggaaagc 396  
Db 256 CCGAATATAGCGACGGGGTCCGACAAACAGAGCCACCGTATCTGGTTACTTGGAAAGC 315

Qy 397 caccggcaagacagacacattcttaagaaagggtgaagctagttgggatgagggaagacatt 456  
Db 316 CACCGAAGAAAGATCGTCAATAATCAGAAAGGAAGCTTGTAGGAATGAGGAA-ACCCT 374

Qy 457 ggtttctatcaagtcagctcctgagccgttaaaacggatggtggtcatgcacgaatt 516  
Db 375 AGTTTTCTATCAGGAAGAGC-CCCAAGGAAGAAAGATGTTGGTGTGATGATCAAT 433

Qy 517 ccgtctccaggatctcatcatcctcccaatctctc---tgagctctccaaaggaga 573  
Db 434 CCGCTTTGATGAAGGTCCTTAGTAACATTCGTTCTCAATTTCTCTCAAGGAGGA 493

Qy 574 ctgggtcttgtaggtatccataaatacgggaaggatttatgtagagacaacat 633  
Db 494 TTGGGTATTATCGCGAGTATTTCACAGAACAAAGAAATTACTTGTCTACCAAGCAGGGAAT 553

Qy 634 gggaagc 640  
Db 554 TGGNAGC 560

RESULT 12  
Bil22890  
LOCUS Bil22890 467 bp mRNA linear EST 31-DEC-2001  
DEFINITION T014P44P Populus leaf cDNA library Populus tremula x Populus tremuloides cDNA, mRNA sequence.

ACCESSION Bil22890  
VERSION Bil22890.1 GI:18006865  
KEYWORDS EST.  
SOURCE Populus tremula x Populus tremuloides.  
ORGANISM Populus tremula x Populus tremuloides.

REFERENCE 1 (bases 1 to 467)  
AUTHORS Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlens, R., Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and Lundberg, J.

TITLE Gene expression in Populus  
JOURNAL Unpublished (2001)

## COMMENT

Contact: Erlandsson R  
Department of Biotechnology  
Royal Institute of Technology  
Teknikringen 30, Stockholm S-10044, Sweden  
Tel: 46 8 790 8287  
Fax: 46 8 245452  
Email: rikeri@biochem.kth.se.

## FEATURES

Location/Qualifiers  
source 1..467  
/organism="Populus tremula x Populus tremuloides"  
/db\_xref="taxon:47664"  
/clone\_lib="Populus leaf cDNA library"  
/note="Organ: leaf"  
BASE COUNT 142 a 93 c 120 g 112 t  
ORIGIN

Query Match 16.6%; Score 213.4; DB 10; Length 467;  
Best Local Similarity 74.0%; Pred. No. 2.4e-28;  
Matches 301; Conservative 0; Mismatches 96; Indels 10; Gaps 2;

Qy 105 agatgaagaagaagtagtataagcattggtggagcaagtgcctccgggattcagatttc 164  
Db 69 AGAGAAAAGATGAGCAACATAAGCTTCGTGGAGGCAAAACTGCCACAGGGTTAGGTTC 128

Qy 165 acccgaagaagcagatgagctgtctgctgattctatgtatgagacgattcacaataatc 224  
Db 129 ATCCAAGAGATGAAGAGCTTGTATGTGATTACTTGATGA-----AGAAGGCTTCTC 179

Qy 225 atcgaccacctcttctcctgattcccaagtgcattcacaagtgtgagccttgggacatcc 284  
Db 180 ACTGGGACTCCCTTCTCATGTAGAGTTCGACCTCAACAAGTGTGAGCTTGGGATATTC 239

Qy 285 caaaaatggcagcgtggaggaaggattgtatttctacagcaaaagacgcaaaat 344  
Db 240 CTGAAACCGCATGCGGTGGAGCAAGGAATGTTACTTTACAGCCAAAGATCGTAAT 299

Qy 345 acgc-gacggggctgagaactaacccgagcaacgacgacgacgacgacgacgacgacgac 403  
Db 300 ATGCAGACTGGACTAAGAACTAATCGAGCAACAGCATCTGGATATTGGAAGCCACCGGT 359

Qy 404 aaagacagaaccattctaaagaaggtaagctagttgggtaggaggaagacattggttttc 463  
Db 360 AAGGACACACATATCTACGTAAAGGAACCCCTTTGGCATGAGAAAGACCTTGGTGTTC 419

Qy 464 latcaagctcagctcctcgcagccgtaaaacccgattgggtcagca 510  
Db 420 TACCAAGTAGGGCACCTTAAGGGNAACCAACCGATTGGGTAATGCA 466

RESULT 13  
BG791220

LOCUS BG791220 588 bp mRNA linear EST 16-MAY-2001  
DEFINITION ESTFN083 Tomato Root Subtraction cDNA Library Lycopersicon esculentum cDNA clone 10G5 5' similar to NAC1, mRNA sequence.

ACCESSION BG791220  
VERSION BG791220.1 GI:14126782  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum

REFERENCE 1 (bases 1 to 588)  
AUTHORS Wang, Y.-H., Garvin, D.F. and Kochian, L.V.  
TITLE Nitrate-induced genes in tomato roots. array analysis reveals novel genes that may play a role in nitrogen nutrition  
JOURNAL Plant Physiol. 127 (1), 345-359 (2001)  
MEDLINE 21437959  
COMMENT Contact: Kochian LV  
US Plant Soil & Nutrition Lab  
Cornell University



Db 215 CTTCTCTTGATAGATGTTGACCTTAACAAGTGTGAGCCATGGGATATTCTCTGAACAGCA 274

QY 296 tgcgtggagggaagattggtattctacagccaaagagacgaagaaatacgcgacgggg 355

Db 275 TGGCTTTGGAGGGAAGGAGTGTATTTCTACACAAAGAGACCGTAAGTATGATCAACACGG 334

QY 356 ctgagactaacgacgaacgacggccacggaatttgaaagccacgcgcgaagacagaaacc 415

Db 335 TTACTCACAATCGTCCACTGCCTCAAGGTATTTGAAGGCCACATGGAAGACAGGCCT 394

QY 416 attctaagaagggttaagctagttggtgaggaagacacattggtttctctatacaaggtcga 475

Db 395 ATCTCCGCAAGGACACCATGATGATGAGTGAAGAACTCTGGTGTACTATCAAGGAAG 454

QY 476 gctcctcgagccgctaaacccgattggttcgacgaattccgtctccaa 526

Db 455 GCACCTCCAGGAGACAAACTGAGTGGTGCATGCATGAGTTTCGTATCGAA 505

RESULT 15

BE554923

LOCUS

DEFINITION

sp82ell.y1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl045-165 5' similar to TR:004017 O04017 CUC2. ;, mRNA sequence.

ACCESSION

BE554923

VERSION

BE554923.1

KEYWORDS

EST.

SOURCE

soybean.

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 441)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 1106 Std Error: 0.00

High quality sequence stop: 419.

Location/Qualifiers

1..441

/organism="Glycine max"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-165"

/clone\_lib="Gm-cl045"

/tissue\_type="Hypocotyl, 9-10 day old etiolated seedlings"

/lab\_host="DH10B"

/note="Vector: pBluescriptII SK+; Site\_1: EcoRI; Site\_2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells

FEATURES

Source

(Gibco BRL). This library was constructed by Dr. Randy Shoemaker.<sup>a</sup>

BASE COUNT 139 a 85 c 117 g 98 t 2 others

ORIGIN

Query Match 16.2%; Score 208; DB 10; Length 441;

Best Local Similarity 72.7%; Pred. No. 2.2e-27;

Matches 298; Conservative 0; Mismatches 102; Indels 10; Gaps 2;

QY 116 agtagtaaacgaggtggaggaagttgcctccggagattccagattcccccgaaggac 175

Db 42 AGCACATACATGCTAGAGGCAAGCTGCCACACAGGATTCAGGTTTCATCCAGAGAT 101

QY 176 gatgagcttgcgtgcgattactgtgagacgattcgttcacaaataatcgcaccacct 235

Db 102 GAAGAGCTTGTGTGTGATTACTTGTATGAAGAAGGTGCAACACATGAT-----TCC 152

QY 236 cttgtcctgatccaaagtcgatctcaacaagtgtgagccttgggacatcccaaaaatggca 295

Db 153 CTTCTCTTGATAGATGTTGACCTTAACAAGTGTGAGGCATGGGATATTCCTGAACACAGCA 212

QY 296 tgcgtggagggaaggtattgtattctacagccaaagagacgaaataacgcgacgggg 355

Db 213 TGCCTGGAGGGAAGGAGTGGTATTTCTACACAAAGAGACCGTAAGTATGCAACAGGG 272

QY 356 ctgagaactaacgagcaacgcgcgcacccggatttggaaagccaccgcgcaagacagaacc 415

Db 273 TTACGCACAAATCGTGCACCTGCCTCAGGGTATTGGAAGGCCACAGGGAAGGACAGSCCT 332

QY 416 attctaagaagggttaagctagttggtgaggaagacattggtttctctatacaggtcga 475

Db 333 ATCTCCGCAAGGACACCCCATGTAGGNATGAGAAAGAC-TTGGTGTTCATCAAGGAAGG 391

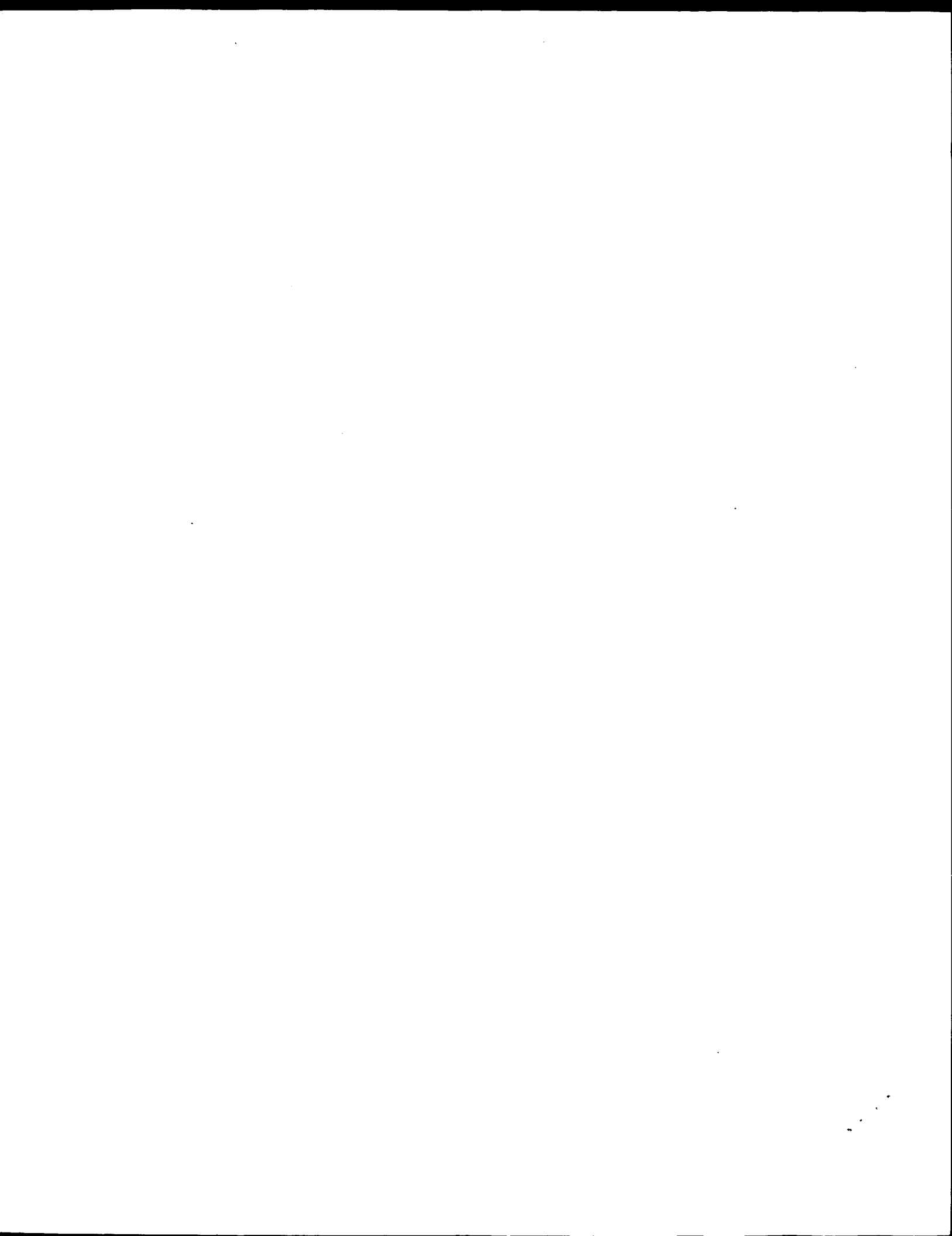
QY 476 gctcctcgagccgtataaacccgattgggttcgacgcaaatccgtctccca 525

Db 392 GCACCCAAAGGGAGAAAACACTGAGTGGGTGCATGCATGAGTTCGTATCGA 441

Search completed: July 15, 2002, 07:07:53

Job time: 1629 sec







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:40:44 ; Search time 199.27 seconds  
(without alignments)  
11088.819 Million cell updates/sec

Title: US-09-889-926-1

Perfect score: 1287

Sequence: 1 gtcgaccacgctcctctt.....aaaaaaaaagggcgccgc 1287

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.\*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.\*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.\*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.\*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.\*
- 6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.\*
- 7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.\*
- 8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.\*
- 9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.\*
- 10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.\*
- 11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1990.DAT.\*
- 12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1991.DAT.\*
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- 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.\*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.\*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.\*
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- 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.\*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.\*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.\*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	1287	21	Arabidopsis thalia
2	1227	95.3	1352	21	Arabidopsis thalia
3	1203	93.5	1351	21	Arabidopsis thalia
4	948.8	73.7	1232	21	Arabidopsis thalia
5	924.4	71.8	1221	21	Arabidopsis thalia
6	176.6	13.7	1179	22	Arabidopsis thalia
7	176.6	13.7	1182	21	Arabidopsis thalia
8	171.8	13.3	1366	21	Arabidopsis thalia
9	171.8	13.3	1481	22	Arabidopsis thalia

10	162	12.6	1321	21	Arabidopsis thalia
11	162	12.6	1352	21	Arabidopsis thalia
12	162	12.6	1355	21	Arabidopsis thalia
13	160	12.4	1358	21	Arabidopsis thalia
14	159.8	12.4	1368	21	Arabidopsis thalia
15	158.6	12.3	1479	22	Arabidopsis thalia
16	158.6	12.3	1485	21	Arabidopsis thalia
17	158.2	12.3	1487	21	Arabidopsis thalia
18	157.8	12.3	1257	21	Arabidopsis thalia
19	156.2	12.1	1198	22	Arabidopsis thalia
20	149.2	11.6	1397	21	Arabidopsis thalia
21	149.2	11.6	1399	21	Arabidopsis thalia
22	148.8	11.6	1192	21	Arabidopsis thalia
23	148.8	11.6	1193	21	Arabidopsis thalia
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25	142.2	11.0	1080	21	Arabidopsis thalia
26	141.6	11.0	1297	21	Arabidopsis thalia
27	140.4	10.9	1082	21	Arabidopsis thalia
28	136.8	10.6	1237	21	Arabidopsis thalia
29	136	10.6	1240	21	Arabidopsis thalia
30	135.6	10.5	1170	21	Arabidopsis thalia
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32	125.2	9.7	1167	21	Arabidopsis thalia
33	125	9.7	1261	21	Arabidopsis thalia
34	125	9.7	1262	21	Arabidopsis thalia
35	122.6	9.5	905	22	Arabidopsis thalia
36	122.6	9.5	1038	21	Arabidopsis thalia
37	122.6	9.5	1042	21	Arabidopsis thalia
38	119.2	9.3	1227	21	Arabidopsis thalia
39	119.2	9.3	1326	21	Arabidopsis thalia
40	119.2	9.3	1326	21	Arabidopsis thalia
41	116	9.0	903	21	Arabidopsis thalia
42	115.8	9.0	1090	20	Arabidopsis thalia
43	112.4	8.7	1680	21	Arabidopsis thalia
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XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
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XX PF 25-FEB-2000; 2000EP-0301439.
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DT 18-OCT-2000 (first entry)		

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KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 13.3%; Score 171.8; DB 21; Length 1366;
Best Local Similarity 62.6%; Pred. No. 6.3e-38;
Matches 320; Conservative 0; Mismatches 182; Indels 9; Gaps 3;

QY 98 gaagaagagatgaagaaatagatataagcatggtgaggaagcaagttgctcgggattc 157
DB 107 gaagaaggtgtgtgtgaatcatggtgaggaagcctgtgtgattgccaactgtttc 166
QY 158 agatttcacccgaagcagcatgctgtctgcgattcttctgatgagacgacgtctcac 217
DB 167 aggtttcatccaacagcagaagagatataacatgtttaccttaag--gagaagggttta 223
QY 218 aataatcatcgaccacaccttctgtctctgatccaagtctgatccaagtgtagccttgg 277
DB 224 aacagcgattcacgctgtgacctggaagcgtgatctcaacagtgtagccttgg 283
QY 278 gacatcccaaaaatggcagcgtggtggaaggaagattggtatttctacagccaaagagac 337
DB 284 gatttgcacaagagggcacaagattggtggggaagagagttctcacttctctgtcacaaggac 343
QY 338 cgaaataacgcagcgggtgagaaactaacccgagcaacggccaccggtatttgaaagcc 397
DB 344 aggaagtatccgactggatgagacgaaccgtgtcgacggagtcaggtactgtgaaagcc 403

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QY 398 accggcaagacagacaccattctaaga---aagggttaagctagtgtggatgaggaagaca 454
DB 404 accgggaagataaggagatcttcaaaagcgaaggttgtctctgttggtggaagaagaaaca 463
QY 455 ttggttttctatcaagtcagtcagtcctcgcgagcgtaaaacccgattgggtcagtcagcaa 514
DB 464 cttgtgtttatagaggaagagctccaaaaggtgaaagactaatgggtcagtcagtaa 523
QY 515 ttccgtctccaagatctcatcatcctcccaatcattctctgagctctccaaagggaagac 574
DB 524 tatcgtcttgaaggcaaatattctgtattacaatc---tcccaaaatctcgaagggaagaa 580
QY 575 tgggtcttgtgtaggtattccataagaata 605
DB 581 tgggtcgtgtgtaggttttttccaagaaca 611

RESULT 9
AAD06453
ID AAD06453 standard; cDNA; 1481 BP.
XX AAD06453;
XX 10-AUG-2001 (first entry)
XX Arabidopsis thaliana transcription factor G526 cDNA.
XX Transcription factor; environmental stress tolerance; gene therapy;
XX plant structure; plant development; ss.
XX Arabidopsis thaliana.
XX Key Location/Qualifiers
XX CDS 181..1188
XX /*tag= a
XX /product= "Arabidopsis thaliana transcription factor"
XX WO200136598-A1.
XX 25-MAY-2001.
XX 14-NOV-2000; 2000WO-US31458.
XX 17-NOV-1999; 99US-0166228.
XX 17-APR-2000; 2000US-0197899.
XX 22-AUG-2000; 2000US-0227439.
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX (PINE/) PINEDA O.
XX (YUGG/) YU G.
XX (CREE/) CREELMAN R.
XX (RIEC/) RIECHMANN J L.
XX (HEAR/) HEARD J.
XX (RATC/) RATCLIFFE O.
XX (REUB/) REUBER L.
XX (KEDD/) KEDDIE J.
XX
XX Pineda O, Yu G, Creelman R, Riechmann JL, Heard J, Ratcliffe O;
XX Reuber L, Keddie J;
XX WPI; 2001-336000/35.
XX P-PSDB; AAE02473.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
XX for altering the environmental stress tolerance characteristics of
XX plants -
XX Claim 4; Page 75-76; 116pp; English.
XX
XX The present sequence is a cDNA encoding Arabidopsis thaliana
XX transcription factor. This novel transcription factor is useful for
XX modifying a plant's phenotype in desirable ways, such as modifying a

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PR 30-JUN-1999; 99US-0141287;
PR 01-JUL-1999; 99US-0141842;
PR 01-JUL-1999; 99US-0142154;
PR 02-JUL-1999; 99US-0142055;
PR 06-JUL-1999; 99US-0142390;
PR 08-JUL-1999; 99US-0142803;
PR 09-JUL-1999; 99US-0142920;
PR 12-JUL-1999; 99US-0142977;
PR 13-JUL-1999; 99US-0143542;
PR 14-JUL-1999; 99US-0143624;
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PR 31-AUG-1999; 99US-0151438;
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PR 10-SEP-1999; 99US-0153070;
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PR 29-OCT-1999; 99US-0162142;

Query Match 12.68; Score 162; DB 21; Length 1321;
Best Local Similarity 61.4%; Pred. No. 3.5e-35;
Matches 296; Conservative 0; Mismatches 180; Indels 6; Gaps 2;

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DB 211 gagcagatggatttaccctcctgggttcagggttcacacacagatgaagaactcataact 270
QY 191 gattactgtgagacgatcgcttcacaaataatcatcgaccacactctgtctctgatccaa 250
DB 271 cactatctccataagaagggttcttgacacca---gcttctcagctaaagctatcggtgaa 327
QY 251 gtcgatctcaacaagtgtgaccttggacatcccaaaatggcatgcgtgggagggaag 310
DB 328 gtgattttaaacaacatcgagccatggaggttaccatgattggcgaataatgggtgagaaa 387
QY 311 gattgtattttacagccaaagacacgaataatcacgcagcggggtgagactaaacga 370
DB 388 gaatggtatttttctgtgtgagagacagaagatctccaccgggtttaagaactaaacga 447
QY 371 gcaacggccacggattattggaagccacccggcgaagacagacacacattcttaagaaagggt 430
DB 448 gcaactgaagccgttattggaagcggacccgggaagagataaagagataaccggggcga 507
QY 431 aagctagttggatgaggaacattggttttctatcaagctgcagctctcctcagggccgt 490
DB 508 tcaactgttggtatgaagaacacactgtttctatagaggaagagctccttaagaggtcag 567
QY 491 aaacccgattgggtcatgcaacgaattccggtctcccaagatcatcatcctcccaatcat 550
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Db 568 aaacccaactgggtgatcatgacaggttgaaagaa---aaattctgtgccataac 624  
QY 551 tctctgaactctcaaaagaactgggtcttctgttaggggtattccataagaatacggaa 610  
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QY 611 gg 612  
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Db 685 gg 686  
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RESULT 11  
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ID AAC41384 standard; DNA; 1352 BP.  
XX AAC41384;  
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XX 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 31686.  
XX Arabidopsis thaliana.  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
PN EP1033405-A2.  
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XX 25-FEB-2000; 2000EP-0301439.  
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PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
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PR 28-OCT-1999; 99US-0162142.

Query Match 12.6%; Score 162; DE 21; Length 1352;  
Best Local Similarity 61.4%; Pred. No. 3.5e-35;  
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QY 131 gtgaggcaaaagtgtcctccgggattccagatttcacccggaaggacgatgagcttgtctgc 190

Db 209 gagcagatggatttacctcctcctgggttcaggtttcacacagatgaagaactcataact 268  
QY 191 gattacttgatgagacgatcgcttcacaataatcatcgaccacctctgtcctgatccaa 250  
Db 269 cactatcctaagaagggtctctgacacca---gttctcagctaagaagtatcgttgaa 325  
QY 251 gtcgatctcaacaagtgtgagccttgggacatcccaaaaatggcatcgttggagggaag 310  
Db 336 gtgtatttaacaaatcagagccatggagttaccatggtgcaaaaatgggtgagaaa 385  
QY 311 gattggtattttctacagcccaaaagagacgcaaaaatacgcgagcggtgagaaactaacga 370  
Db 386 gaatggtatttttctgtgagagacagaagaagtatccaccgggtttaagaactaacga 445  
QY 371 gcaacggccaccggatattgaaagccaccggcaaaagacagacacattcttaagaaaggt 430  
Db 446 gcaactgaagccggttatttgaagcgaccgggaagataaagagataaccagggcaaa 505  
QY 431 aagctagttggatgaggaagacatttggtttctatcaagtcgagctcctcagggcgt 490  
Db 506 tcacttgttggatgaggaagacacacttgtttctatagaggaaagagctcctaaaggtcag 565  
QY 491 aaaaccgatgggtcagcagcaaatccgtctccaaagatctcatcatcctcccaatcat 550  
Db 566 aaaaccaactgggtgatgcatgagtacaggcttgaagga---aaattctctgccatac 622  
QY 551 tctctgagctctccaaaggaagactgggtcttgtgtaggtattccataagaatacagaa 610  
Db 623 ttgccgaaaaaccgcaagaagaatgaatgggtgatcaggggtgttcccaaaagagtgtcggg 682  
QY 611 gg 612  
Db 683 gg 684  
  
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ID AAC48786 standard; DNA; 1355 BP.  
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AC AAC48786;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58765.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
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PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-0301439.  
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PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 12.6%; Score 162; DB 21; Length 1355;  
Best Local Similarity 61.4%; Pred. No. 3.6e-35;  
Matches 296; Conservative 0; Mismatches 180; Indels 6; Gaps 2;

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Db 386 gaattgtattttctgtgtgagagacagaagaatccaccggttttaagaactaacgga 445  
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QY 431 aagctagttggatgagggaagcattggtttctctatcaaggtcgagctcctcgcgcgt 490  
Db 506 tcactgttggatgagaagacactgtttctctatagaggagagcctcctaaagggtcag 565  
QY 491 aaaaacgattgggtcagcagaattccgtctccaggatctcatcctcccaatcat 550  
Db 566 aaaaacactgggtgatgacaggttgagga---aaattctctgcccataac 622  
QY 551 tctctgagctctccaaagaagactgggtctgtgtagggtattccataaagaatacggaa 610  
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Db 683 gg 684

## RESULT 13

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ID AAC40896 standard; DNA; 1358 BP.

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AC AAC40896;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29918.

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KW Hybridisation assay; genetic mapping; gene expression control;

protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
OS EP1033405-A2.  
PN 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-0301439.  
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PR 05-MAR-1999; 99US-0123180.  
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PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
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PR 30-APR-1999; 99US-0132048.  
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PR	23-AUG-1999;	99US-0149902.			
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PR	27-AUG-1999;	99US-0151080.			
PR	30-AUG-1999;	99US-0151303.			
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PR	07-SEP-1999;	99US-0152363.			

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12.4%; Score 160; DB 21; Length 1358;

Best Local Similarity 61.2%; Pred. No. 1.3e-34;

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QY	191	gattacttgatgagacgatcgcttccacaataatcatcgaccaccttgtctctgatccaa	250
Db	271	cactatctccataagaagggtcttgacacca---gcttctcagctaaagctatcggtgaa	327
QY	251	gtcgatctcaacaagtgtgagccttgggacatcccaaaaatggcatgcgtgggagggaag	310
Db	328	gttgatttaacaaatcagagccatggtgagttacctatggtgcaaaaatggtgagaaa	387
QY	311	gattggatttctacagccaaagagaccgcaaaaatacgcagcggggctgagaaactaacga	370
Db	388	gaatgggtattttctgtgtgagagacagaagaagtatcccacgggtttaaagaactaacga	447
QY	371	gcaacgcccacgggatatttgaaagccacccgcaaaagacagaccatttctaagaaggt	430
Db	448	gcaactgaagccgggttatctggaggcgcgggaaggataaagagatataccgagggcaaa	507
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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6

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TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-Fls
US-08-232-463-14

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Best Local Similarity 4.1%; Pred. No. 0.0032;
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; Sequence 1, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
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RESULT 5
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; Sequence 1, Application US/08999774A
; Patent No. 6274312
; GENERAL INFORMATION:
; APPLICANT: Gish, Kurt C.
; APPLICANT: Seghezzi, Wolfgang
; APPLICANT: Shanahan, Frances
; APPLICANT: Lees, Emma M.
; APPLICANT: McClanahan, Terrill K.
; TITLE OF INVENTION: Intracellular Regulatory Molecules;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/999,774A
; FILING DATE: 10-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,818
; FILING DATE: 11-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4081 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 117..3431
; IS-08-999-774A-1

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US-09-232-200-36
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Query Match      2.7%; Score 35.2; DB 4; Length 2885;
Best Local Similarity 68.1%; Pred. No. 0.93;
Matches 49; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
```

```
QY 1216 tagacatacatatttcacgtcgttagttccattgtttcaaaaaaaaaaaaaaaaaaa 1275
    || || || || || || || || || || || || || || || || || || || || ||
Db 2814 taaaatttctaatttgaataaaagattaaattttactgaaaaaaaaaaaaaaaaaa 2873
```

```
QY 1276 aaggcgccgcgc 1287
    | |||||
Db 2874 attggcgccgc 2885
```

```
Search completed: July 15, 2002, 07:09:09
Job time: 1705 sec
```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 06:55:13 ; Search time 17.76 Seconds  
(without alignments)  
1752.981 Million cell updates/sec

Title: US-09-889-926-2

Perfect score: 1757

Sequence: 1 METEEMKRESSISMVEAKLP.....EGSSESLTLDIGIPSTVWNC 324

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1579.5	89.9	309	C96601	hypothetical prote
2	536.5	30.5	334	T04050	unknown protein Fl
3	505.5	28.8	316	E84636	NAM (no apical mer
4	491.5	28.0	365	G84559	probable NAM (no a
5	473	26.9	298	H96584	hypothetical prote
6	472.5	26.9	334	T47983	hypothetical prote
7	470.5	26.8	324	B96742	NAM-like protein -
8	459.5	26.2	399	T02678	NAM (no apical mer
9	456	26.0	377	T04585	hypothetical prote
10	456	26.0	418	E86395	hypothetical prote
11	453.5	25.8	631	D96683	hypothetical prote
12	446.5	25.4	341	T04050	hypothetical prote
13	439	25.0	320	A96570	NAM-like protein,
14	438.5	25.0	358	E86452	protein F6N18.15 [
15	436.5	24.8	317	B96570	NAM-like protein,
16	436	24.8	300	H96636	hypothetical prote
17	436	24.8	314	T09933	hypothetical prote
18	436	24.8	409	G86257	hypothetical prote
19	434	24.7	305	F86456	unknown protein [i
20	429	24.4	253	G96803	GRAB1-like protein
21	423.5	24.1	303	T52345	OSNAC6 protein [im
22	421	24.0	289	E86148	TING.12 protein -
23	420	23.9	329	T52344	-OSNAC5 protein [im
24	413.5	23.5	534	T04663	hypothetical prote
25	411	23.4	268	T52343	hypothetical prote
26	410.5	23.4	567	T48437	hypothetical prote
27	397.5	22.6	275	G84860	NAM (no apical mer
28	395	22.5	262	T05084	hypothetical prote
29	390.5	22.2	268	A84746	probable NAM (no a

30	378.5	21.5	315	2	T04624	hypothetical prote
31	374	21.3	283	2	F96450	hypothetical prote
32	370	21.1	272	2	T07182	hypothetical prote
33	366	20.8	276	2	D84547	NAM (no apical mer
34	363	20.7	176	2	G84436	NAM (no apical mer
35	362	20.6	335	2	C84671	NAM (no apical mer
36	361.5	20.6	557	2	B86466	hypothetical prote
37	358.5	20.4	576	2	A86466	hypothetical prote
38	347.5	19.8	469	2	T46230	hypothetical prote
39	336	19.1	335	2	T49145	hypothetical prote
40	326	18.6	522	2	E86453	CDS protein F9L11.
41	309	17.6	220	2	T52100	ATAF2 protein - Ar
42	292.5	16.6	229	2	T52342	NAC-domain protein
43	283.5	16.1	229	2	S37101	ATAF1 protein - Ar
44	273.5	15.6	457	2	B85020	probable NAM-like
45	255	14.5	302	2	T01942	hypothetical prote

#### ALIGNMENTS

RESULT 1

C96601

hypothetical protein T6H22.19 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: C96601

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: C96601

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-309 <STO>

A:Cross-references: GB:AB005173; NID:96056383; PIDN:AAF02847.1; GSPDB:GN00141

C:Genetics:

A:Gene: T6H22.19

A:Map position: 1

Query Match 89.9%; Score 1579.5; DB 2; Length 309;  
Best Local Similarity 91.8%; Pred. No. 1.9e-129;  
Matches 302; Conservative 0; Mismatches 2; Indels 25; Gaps 3;

QY 1 METEEMKRESSISMVEAKLPQGFPHPKDDELVC DYLMRRSLHNNHRRPPLVLIQVDLNKC 60

|||||

Db 1 METEEMKRESSISMVEAKLPQGFPHPKDDELVC DYLMRRSLHNNHRRPPLVLIQVDLNKC 60

|||||

QY 61 EPWDIP----KMACVGKDWYFYSDRDKVATGRTNRATATGYKATGKDRITLRGK 115

|||||

Db 61 EPWDIPMNTTKRVC-----QDRKATGRTNRATATGYKATGKDRITLRGK 111

QY 116 LVGMKRTLVFYOGRAPRGKTDWVMHEFRLOQSHPPNHSLSPPKEDVWLRFVHKNFEG 175

|||||

Db 112 LVGMKRTLVFYOGRAPRGKTDWVMHEFRLOQSHPPNHSLSPPKEDVWLRFVHKNFEG 160

|||||

QY 176 VTCRNMGSCFDETSASLPPLMDPYINFDOEPSYLSDDHHYIINEHVPCFNSLSONQT 235

|||||

Db 161 VICRNMGSCFDETSASLPPLMDPYINFDOEPSYLSDDHHYIINEHVPCFNSLSONQT 220

|||||

QY 236 LNSNLTNSVSELKIPCKNPPLFTGGSASATLTGLDSCSSDQWVLRALLSQLKIDGSL 295

|||||

Db 221 LNSNLTNSVSELKIPCKNPPLFTGGSASATLTGLDSCSSDQWVLRALLSQLKIDGSL 280

|||||

QY 296 GPKESQSYGEGSSESLTLDIGIPSTVWNC 324



Db 123 P N G K K S D W I M H E V R L E S D E N A P ----- P Q E G W V V C R A F K K R A T G O A K N T E T W S S Y I V 176  
QY 187 D E T A S A L P L M D P Y I N F D O E P S S Y L S D D H Y I I N E H V P C F S N L S Q N O T L N S L T N S V S E 246  
Db 177 D E V A P N G V N S V M D P I ----- D Y I S K O O H N I F G R G L M C K Q E L - E G M V D G I N Y I Q S N O F 227  
QY 247 L K I P - C K N P N - P L F T G S S A S A T L T G L D S 272  
Db 228 I Q L P Q L O S P S L P L M K R P S S M S I T S M D N 255

## RESULT 5

H96584  
hypothetical protein F20D21.15 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: H96584  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96584  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <STO>  
A:Cross-references: GB:AE005173; NID:g4585977; PIDN:AA25613.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F20D21.15  
A:Map position: 1

Query Match 26.9%; Score 473; DB 2; Length 298;  
Best Local Similarity 40.1%; Pred. No. 2.2e-33;  
Matches 112; Conservative 26; Mismatches 61; Indels 80; Gaps 10;

QY 19 L P P G F R H P K D D E L V C D Y L M R S L N H R P P L V L I - Q V D L N K C E P W D I P K M A C V G K D - - 75  
Db 3 L P P G F R H P D E L V A Y L D R K V - N G A L E L I P E V D L Y K C E P W D L P E K S F L P G N D M E 60  
QY 76 W Y F Y S Q R D K R Y A T G L T N R A T A G Y W K A T G K D R T I L R K G L V G M R K T L V Y O G R A P R G R K 135  
Db 61 W Y F Y S T R K Y P N G S T N R A T A G Y W K A T G K D R T V E S K K M G M K K T L V Y R G R A P H G L R 120  
QY 136 T D W M H E F R L O G S H P P N H S L S P K E D W L C R V F H K N - - - - - 172  
Db 121 T N W M H E Y R L T - - - H A P S S L - - - K E S Y A L C R V F K K I O I P R K K G E E E A E E S T V S V G K E 174  
QY 173 - - - - - T E G V I C R D - - - - - N M G S C F D E T A S A L P L M D P Y I N F D Q 206  
Db 175 E E E E K K W R K C D G N Y I E D S L K R A S A E T S S E L T G V L L D E A N S S I - - - - - F A L 225  
QY 207 E P S S Y L S D D H Y I I N E - - - - - H V P C - - - - - F S N L S Q N Q 234  
Db 226 H F S S L L D D H D L F S N Y S H Q L P Y H P P L Q L Q D F P L S M N E 264

## RESULT 6

T47983  
NAM-like protein - Arabidopsis thaliana  
N:Alternate names: protein F21F14.80  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T47983  
R:Cholsne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa  
submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24481  
A:Accession: T47983  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-334 <CHO>  
A:Cross-references: EMBL:AL138642  
A:Experimental source: cultivar Columbia; BAC clone F21F14  
C:Genetics:  
A:Map position: 3  
A:Introns: 58/1  
A:Note: F21F14.80

Query Match 26.9%; Score 472.5; DB 2; Length 334;  
Best Local Similarity 33.1%; Pred. No. 2.8e-33;  
Matches 119; Conservative 52; Mismatches 89; Indels 99; Gaps 15;

QY 16 E A K L P P G F R H P K D D E L V C D Y L M R S L N H R P P L V L I Q V D L N K C E P W D I P K M A C V G - - - 72  
Db 8 Q S O V P P G F R H P T E E L L - K Y L R K K I S N I K I D L D V I P D I D L N K L E P W D I Q E M C K I G T T P 66  
QY 73 G K D W T F Y S Q R D K R Y A T G L T N R A T A G Y W K A T G K D R T I L R K G L V G M R K T L V Y O G R A P R 132  
Db 67 Q N D W T F Y S H K D K Y P T G T R T N R A T V G F W K A T G R D K T I Y T N G D R I G M R K T L V Y F Y K G R A P H 126  
QY 133 G R K T D W M H E F R L Q - - - - - G S H - - H P P N H S L S P K E D W L C R V F H K N T E G V I C R D N M 182  
Db 127 G O K S D W I M H E F R L D E S V L I S C G D H D V N V E T C D V I G S D E G W V V C R V F K N N - - - L C K N M I 183  
QY 183 G S - - - - - C F D E T A S A L P L M - - - - - D P Y I N F D Q E P S S Y L S D D H Y I I N E H 223  
Db 184 S S P A S S V K T P S F N E E T I E Q L L E V M G S C K G E I V L D P L K L - - - - - P N 226  
QY 224 V P C F S N - - L S O N O T L N S L T N S - - V S E L K I P C K N P N L F T G G S A S A L T G L D S C S D Q M 279  
Db 227 L E C H N N T T I T S Y O M L I D D Q V N N C H V S K Y M D P - - - - - S F I T S W A A 265  
QY 280 V L R A L L S O L T K I D G S L G P - - - - - K E S Q S V G - - - E G S S E S L L T D I G I P S - T W N 323  
Db 266 L D R L V A S Q L N - - - - - G P N S Y S I P A V N E T S O S P Y H G L N R S C N T G L T P D Y I P E I D L W N 318

## RESULT 7

B96742  
NAM-like protein, 48543-50167 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B96742  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: B96742  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-324 <STO>  
A:Cross-references: GB:AE005173; NID:g6978918; PIDN:AAF34310.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F17M19.8  
A:Map position: 1

Query Match 26.8%; Score 470.5; DB 2; Length 324;  
Best Local Similarity 35.1%; Pred. No. 4e-33;  
Matches 107; Conservative 52; Mismatches 75; Indels 71; Gaps 10;



E86395<sup>4</sup>

hypothetical protein T2P19.6 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001

C:Accession: E86395

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

Nelson, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: E86395

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-418 &lt;STO&gt;

A:Cross-references: GB:AE005172; NID:g4262176; PIDN:AAD14493.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 26.0%; Score 456; DB 2; Length 418;

Best Local Similarity 34.4%; Pred. No. 1e-31;

Matches 128; Conservative 42; Mismatches 112; Indels 90; Gaps 16;

QY 15 VEAKLPGRFPHKDDDELVCYLMRSLHNNRPPL---VLIQVDLNKCEPWPDPKMACV 71

D 12 MEDVLLPGFRFHPHTDEELVYLYLKRKQHN---PLSIELIQLDLYKYDPPDLPRFAMT 67

QY 72 GGDWYFYSDRDKRYATGLRTNATATGYWKATGKDTILRK--GKLVGMKRTLVFYQGR 129

D 68 GEKWIYCYPRDKRYNRRSPNRVTGAGFWKATGTRDPIYSSGNCIGLKRSLVIFYGR 127

QY 130 APRGKTDWMHFRLO--GSHHPN---HSLSPKEDWVLCRVFHKNTGIVICRDNMG 183

D 128 AAKGVKTDWMHFRLOPSLSEPPSKRRFPDPSVPSPNDWAICRIFKKTNTTL----- 181

QY 184 SCFETASASLPP--LMDPIYDFQEPSSYLSD-----HYIIN----- 221

D 182 RALSHSVSSLLPTSTDTMSNQSNTHYFSSDKILKPSHFQFHNNMTPTKSTNT 241

QY 222 EHVPCFNLNLS---NQTLNSLNTNSVSEL-----KIPCKNPPL 257

D 242 PSVPTISPFYLDFTSYDKPTNFVNPVSCLDQOYLNLFLATQETQPPPLPSNEIFS 301

QY 258 FTGGSASATLTGLDSFCSSQDQVLRALLSQ-----LTKIDGSLGPKESQSYG----- 304

D 302 FLNLTSSDS--TFLGEFTS--HIDLSAVLAQEQCPPLVSL-----POEYQETGFEANGIMK 353

QY 305 --EGSSSESLTD 314

D 354 NMRGSNEDHLGD 365

RESULT 11

D96683

hypothetical protein F12P19.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: D96683

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

Nelson, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: D96683

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-631 &lt;STO&gt;

A:Cross-references: GB:AE005173; NID:g6227016; PIDN:AAF06052.1; GSPDB:GN00141

C:Genetics:

A:Gene: F12P19.8

A:Map position: 1

Query Match 25.8%; Score 453.5; DB 2; Length 631;

Best Local Similarity 34.9%; Pred. No. 2.9e-31;

Matches 112; Conservative 35; Mismatches 97; Indels 77; Gaps 10;

QY 14 MVEAKLPGRFPHKDDDELVCYLMRSLHNNRPPLVLI-QVDLNKCEPWPDPKMACVG 72

D 1 MAPVSMPPGFRFHPHTDEELVYLYLKRKI--NGRTIELEIPIIDLYKCEPWPDPKSLLP 58

QY 73 GKD--WYFYSDRDKRYATGLRTNATATGYWKATGKDTILRKGLVGMKRTLVFYQGR 130

D 59 SKDLEWFFSPDRKYPNGRNTRATKAGYWKATGKDRKVTSHRMVGTGKTLVYIRGRA 118

QY 131 PRGKTDWMHFRLOQSGSHHPNHSLSPPKEDWVLCRVFHKNTGIVICRDNMGSCFDETA 190

D 119 PHGSRDWMHFRLE---EQECDSKSGIQDAYALCRVFKKSA----- 158

QY 191 SASLPLMDPYINFDOEPSSYLSDDHHYIINEHVPCFNSLSONQTLNSLNTNSVSELKIP 250

D 159 -----LANKIEQHH-----GTTKKNKGTNTNSEQSTST 186

QY 251 CKNPNPLF-----TGGSASATLTGLDSFCSSQDQVLRALLSQTLLKIDGSLG- 296

D 187 CLYSDGMVENLENSGYPVSPETGG-----LTQLGNSSDMETIENKKSQPMASHDTSPNF 241

QY 297 PKESQSYGEGSSESLTDIGI 317

D 242 PPQSQ-YGTISYPPSKVDIAL 261

RESULT 12

T04050

hypothetical protein F24G24.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 30-Apr-1999

C:Accession: T04050

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15184

A:Molecule type: DNA

A:Residues: 1-341 &lt;BEV&gt;

A:Cross-references: EMBL:AL049488

A:Experimental source: cultivar Columbia; BAC clone F24G24

C:Genetics:

A:Map position: 4

A:Introns: 56/1: 148/3

A:Note: F24G24.150

Query Match 25.4%; Score 446.5; DB 2; Length 341;

Best Local Similarity 52.9%; Pred. No. 5.2e-31;

Matches 83; Conservative 27; Mismatches 38; Indels 9; Gaps 4;

QY 19 LPPGFRFPHKDDDELVCYLMRSLHNNRPPLVLIQVDLNKCEPWPDPKMACVG---KD 75

D 9 VPPGFRFPHKDDDELVCYLMRSLHNNRPPLVLIQVDLNKCEPWPDPKMACVG---KD 67

QY 76 WYFYSDRDKRYATGLRTNATATGYWKATGKDRKTLRKGLVGMKRTLVFYQGRAPGRK 135

D 68 WYFHSKDRKRYATGLRTNATATGYWKATGKDRKTLRKGLVGMKRTLVFYQGRAPGRK 127

QY 136 TDWVMEFRFQSGHHPPNLSLSPKED-VWLCRVFHK 171  
||||:||||: | : : : |||:|||| |  
Db 128 TDWIMHEYRLDADDPO-----ANPSDGGWVCRVFMK 160

## RESULT 13

B96570

NAM-like protein, 59502-58357 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: A96570

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talton,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: A96570

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-320 &lt;STO&gt;

A:Cross-references: GB:AE005173; NID:g6862948; PIDN:AAF30336.1; GSPDB:GN00141

C:Genetics:

A:Gene: F14G24.15

A:Map position: 1

Query Match 25.0%; Score 439; DE 2; Length 320;

Best Local Similarity 32.3%; Pred. No. 2.1e-30;

Matches 101; Conservative 44; Mismatches 82; Indels 86; Gaps 9;

QY 16 EAKLPGRFPHKDELVCYLMRSLHNNRPPVLVQLVDLNKCEPMDIPKMACVGGKD 75

Db 14 QNPLPGFRFHTDESLVTHYLKRA-DVPLPVAIIADVDLYKDFDPWELPAKASFSGQE 72

QY 76 WYFYSQRDKYATGLRTNRATATGYWKATGKDTILRKG-----KLVGMRKTLVFFYQGRAP 131

Db 73 WYFFSPDRKYPNGARPNRAATSGYWKATGDKPVISGGGSKVKYKALVFGSRPP 132

QY 132 RGRKTDWVMEFRFQSGHHPPNH-----SLSSPKEDWLCRVFHKNTGVCICRDNMGS 184

Db 133 KGVKSDWIMHEYRL--TDNKPTHICDFGNKNSLRDLCEWLCRIYKN----- 178

QY 185 CFDEASASLPLMDPYINFDQEPSSYLSDDHHYIINHPV----- 225

Db 179 --NSTASRHHHLHLHLHLDNRHDMIDDRF---RHVPGLHFPALFSDNDPTAIY 233

QY 226 -----CFNSLSONQL-----NSLNTSVSELKIPCKNPPL 257

Db 234 DGGGGYGGGYSNMHCFFASGSKQQLFPPVMMTSLNQDSIGSSS-----PSKR 285

QY 258 FTGGSASATLTGL 270

Db 286 FNGGGVGDGCTSM 298

## RESULT 14

E86452

protein F6N18.15 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: E86452

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: E86452  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358 <STO>  
A:Cross-references: GB:AE005172; NID:g6714280; PIDN:AAF25976.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F6N18.15  
A:Map position: 1

Query Match 25.0%; Score 438.5; DB 2; Length 358;  
Best Local Similarity 33.4%; Pred. No. 2.8e-30;  
Matches 107; Conservative 61; Mismatches 105; Indels 47; Gaps 11;

QY 16 EAKLPGRFPHKDELVCYLMRSLHNNRPPVLVQLVDLNKCEPMDIPKMACVGG-- 73

Db 13 QSKVPPGFRFHTDEELL-HYLRKKVNSQKIDLDVIREVDLNKLEPMDIQECRICGSP 71

QY 74 -KDWYFSQRDKYATGLRTNRATATGYWKATGKDTILRKGKLVGMKTLVFFYQGRAP 132

Db 72 QNDWYFFSHKDKKPYTGRNRAFVAGWRATGDKLICSVRRIGLRKTLVFFYKGRAPH 131

QY 133 GRKTDWVMEFRFQSGHHPPNH-----LSSPKEDWLCRVFHKNTGVCICRDNMGS 185

Db 132 GQKSDWIMHEYRLDTPMSNGYADVVTEDPMSYNEGGWVCRVFRKKNYQKI----- 183

QY 186 FDEASASLPLMDPYINFDQEPSSYLSDDHHYIINHPVCF-----SNL-----SONQL 236

Db 184 -DCPKITLSSLPD---DTEEEKGPTFHNTQNTGLDHLVLLYMDRTGSCNICMPESQTTQ 239

QY 237 NSN--LNTSVSELKIPCKNPPLFTGGSASATLTGLDSCSDQVLRALLSOLTKID-- 292

Db 240 HODVLFMQLPSLETP--KSESPV---DQSLFPLSKLDFSPVQEKITERPCVSNWASLDRL 295

QY 293 -----GSLGPKESQSYGE 305

Db 296 VAWQLNNGHHNCPCHKRSFDE 315

## RESULT 15

B96570

NAM-like protein, 67516-66364 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: B96570

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: B96570

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-317 &lt;STO&gt;

A:Cross-references: GB:AE005173; NID:g6862949; PIDN:AAF30337.1; GSPDB:GN00141

C:Genetics:

A:Gene: F14G24.16

A:Map position: 1

Query Match 24.8%; Score 436.5; DB 2; Length 317;

Best Local Similarity 32.9%; Pred. No. 3.5e-30;



Search completed: July 15, 2002, 06:57:27  
Job time: 134 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:56:48 ; Search time 13.42 Seconds  
(without alignments)  
934.809 Million cell updates/sec

Title: US-09-889-926-2

Perfect score: 1757

Sequence: 1 METEEMKRESSISMVEAKLP.....EGSSBSLLTDIGIPSTVWNC 324

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	6.0	1872	1 T2D1_HUMAN	P21675 homo sapien
2	95	5.4	3092	1 IRAL1_YEAST	P18963 saccharomyc
3	95	5.4	3969	1 HRX_HUMAN	Q03164 homo sapien
4	87.5	5.0	314	1 Y009_HUMAN	Q15390 homo sapien
5	87.5	5.0	928	1 PM11_CHLPN	O86164 chlamydia p
6	87.5	5.0	3866	1 HRX_MOUSE	P55200 mus musculu
7	86.5	4.9	1377	1 CID_DROME	P19538 drosophila
8	85	4.8	530	1 GP2_RAT	P19218 rattus norv
9	85	4.8	610	1 UVRC_ECOLI	P07028 escherichia
10	84.5	4.8	429	1 NPT1_YEAST	P39683 saccharomyc
11	84.5	4.8	1182	1 HAIR_MOUSE	O61645 mus musculu
12	84.5	4.8	1458	1 PA2R_RABIT	P49260 oryctolagus
13	83.5	4.8	337	1 YDTB_SCHPO	O14216 schizosacch
14	83.5	4.8	591	1 IF37_ARATH	P56820 arabidopsis
15	82.5	4.7	584	1 ENV_IPMAE	P31789 mouse intra
16	82	4.7	584	1 YBX1_SCHPO	Q10207 schizosacch
17	81.5	4.6	1181	1 HAIR_RAT	P97609 rattus norv
18	81.5	4.6	2222	1 CCAE_RAT	Q07652 rattus norv
19	81	4.6	271	1 VA04_VARV	P33832 variola vir
20	81	4.6	3125	1 POLG_PPVNA	P17766 p genome po
21	80	4.6	368	1 VE2_HP45	P36794 human papil
22	80	4.6	894	1 FOX2_NEUCR	Q01373 neurospora
23	80	4.6	1142	1 MGCI_HUMAN	O60732 homo sapien
24	79.5	4.5	454	1 MUC_HUMAN	P01871 homo sapien
25	79.5	4.5	510	1 YD85_SCHPO	Q10410 schizosacch
26	79.5	4.5	765	1 AMDR_EMENI	P15699 emericeella
27	79.5	4.5	969	1 AGLU_SCHPO	Q9c0y4 schizosacch
28	79.5	4.5	1117	1 YN96_YEAST	P53753 saccharomyc
29	79.5	4.5	1210	1 ICEN_PSEFL	P09815 pseudomonas
30	79	4.5	356	1 POU1_XENLA	P31363 xenopus lae
31	79	4.5	458	1 YW51_YEAST	P42933 saccharomyc
32	79	4.5	479	1 XYL4_HORVU	Q40082 hordeum vul
33	79	4.5	711	1 RED1_RAT	P51400 rattus norv

## ALIGNMENTS

RESULT	1
T2D1_HUMAN	
ID	T2D1_HUMAN
AC	P21675
DT	01-MAY-1991 (Rel. 18, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)
DE	Transcription initiation factor TFIID 250 kDa subunit (TAFII-250)
DE	(TAFII250) (TBP-associated factor 250 kDa) (P250) (Cell cycle gene 1 protein).
GN	TAF2A OR CCG1 OR BA2R.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Laryngeal carcinoma;
RX	MEDLINE=91246200; PubMed=2038334;
RA	Sekiguchi T., Nohiro Y., Nakamura Y., Hisamoto N., Nishimoto T.;
RT	"The human CCG1 gene, essential for progression of the G1 phase, encodes a 210-kilodalton nuclear DNA-binding protein.";
RL	Mol. Cell. Biol. 11:3317-3325(1991).
RN	[2]
RP	PRELIMINARY SEQUENCE FROM N.A.
RX	MEDLINE=89005056; PubMed=3169001;
RA	Sekiguchi T., Miyata T., Nishimoto T.;
RT	"Molecular cloning of the cDNA of human X chromosomal gene (CCG1) which complements the temperature-sensitive G1 mutants, tsBN462 and ts13, of the BHK cell line.";
RT	EMBO J. 7:1683-1687(1988).
RN	[3]
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX	MEDLINE=93196704; PubMed=7680771;
RA	Ruppert S., Wang E.H., Tjian R.;
RT	"Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation.";
RL	Nature 362:175-179(1993).
RN	[4]
RP	CHARACTERIZATION.
RX	MEDLINE=93196705; PubMed=8450888;
RA	Hisatake K., Hasegawa S., Takada R., Nakatani Y., Horikoshi M., Roeder R.G.;
RT	"The P.50 subunit of native TATA box-binding factor TFIID is the cell-cycle regulatory protein CCG1.";
RL	Nature 362:179-181(1993).
CC	-!- FUNCTION: MAY PLAY AN ESSENTIAL ROLE IN TFIID ASSEMBLY BY INTERACTING WITH BOTH TBP AND OTHER TAF, AS WELL AS SERVING TO LINK THE CONTROL OF TRANSCRIPTION TO THE CELL CYCLE. ESSENTIAL FOR PROGRESSION OF THE G1 PHASE OF THE CELL CYCLE. POSSESSES DNA-BINDING ACTIVITY.
CC	-!- SUBUNIT: TFIID IS COMPOSED OF TBP AND A VARIETY OF TBP-ASSOCIATED FACTORS.
CC	-!- SUBCELLULAR LOCATION: Nuclear.
CC	-!- PTM: PHOSPHORYLATED BY CASEIN KINASE II IN VITRO.
CC	-!- SIMILARITY: CONTAINS 2 BROMODOMAINS.

34	79	4.5	726	1	K182_YEAST	P25341 saccharomyc
35	79	4.5	971	1	CLA4_CANAL	O14427 candida alb
36	79	4.5	4655	1	LRP2_HUMAN	P98164 homo sapien
37	78.5	4.5	468	1	PCO1_MOUSE	O61398 mus musculu
38	78.5	4.5	478	1	ARDE_CHLMU	P56961 chlamydia m
39	78.5	4.5	978	1	SIR3_YEAST	P06701 saccharomyc
40	78.5	4.5	1468	1	NI53_RAT	P49791 rattus norv
41	78	4.4	391	1	MUCB_HUMAN	P04220 homo sapien
42	78	4.4	837	1	STA6_MOUSE	P52633 mus musculu
43	78	4.4	2182	1	CABL_RAT	O88480 rattus norv
44	77.5	4.4	181	1	BY55_HUMAN	O95971 homo sapien
45	77.5	4.4	590	1	YNW7_YEAST	P53863 saccharomyc

CC -!- SIMILARITY: CONTAINS 1 HMG BOX.  
 CC -!- SIMILARITY: TO DROSOPHILA TAFII-230. SOME TO S.POMBE TAFII-111  
 CC AND TO S.CEREVISIAE TAFI45.  
 CC -----  
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 CC -----  
 CC EMBL; D90359; BAAL4374.1; -;  
 CC EMBL; X07024; CAA30073.1; ALT\_SEQ.  
 CC PIR; S03005; S03005.  
 CC PIR; A40262; A40262.  
 CC TRANSFAC; T02206; -;  
 CC MIM; 313650; -;  
 CC InterPro; IPR001487; Bromodomain.  
 CC Pfam; PF00439; bromodomain; 2.  
 CC PRINTS; PR00503; BROMODOMAIN.  
 CC SMART; SM00297; BROMO; 2.  
 CC PROSITE; PS00633; BROMODOMAIN\_1; 2.  
 CC PROSITE; PS50014; BROMODOMAIN\_2; 2.  
 CC Bromodomain; Nuclear protein; DNA-binding; Cell cycle; Repeat;  
 KW Transcription regulation; Phosphorylation.  
 FT DOMAIN 157 165  
 FT PRO-RICH.  
 FT DNA\_BIND 1195 1273 HMG BOX (POTENTIAL).  
 FT DOMAIN 1351 1358 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 1397 1467 BROMODOMAIN 1.  
 FT DOMAIN 1520 1590 BROMODOMAIN 2.  
 FT DOMAIN 1627 1872 ASP/GLU-RICH (ACIDIC TAIL).  
 SQ SEQUENCE 1872 AA; 212676 MW; 93BE3D181A72ABEB CRC64;

Query Match 6.0%; Score 106; DB 1; Length 1872;  
 Best Local Similarity 19.9%; Pred. No. 0.37;  
 Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

QY 1 MTEEEKKSS--ISMVEAKLP-----GFRFHPKDDDELVDYLMR--RSLFNHRRPPL 50  
 Db 1330 IESADEVRKSLVLKFPKQOLPKKRRVGTTH-----CDYLRPHKSIHRRTPDM 1382  
 QY 51 VLQV-----DLNCKEPWDIPKACVGKDWYFYSQRDRKYATGLRNRATATGY 100  
 Db 1383 VTLSSILEINDMRDLNTPYPTHTPVNAKV-VKDYKIIITRPMDLQT-LREN----- 1433  
 QY 101 WKATGKDRITLRKGLVGRKTLVFFYQGRAPGRKTDWVWHEFR-----LQGSHP 152  
 Db 1434 -----VKRL--YPSR-----EEREHLELVKNSATYNGP 1462  
 QY 153 NLSLSPKEDWV-LCRVFHKNTEGVICRDNMGSCFDEITASLPLMDPYINFDOEPSSY 211  
 Db 1463 KHSITQISQSLDCLDEKLEKEDKLAR-----LEKAINPLD---DDQVATFSF 1509  
 QY 212 LSDD-----HHYIINHVPFCFNSLSON-----OTLNSNLT----- 241  
 Db 1510 ILDNIVTQKMAVPDSWPFHPHVKFVDPYKVIYNPMDLETIRKNISKHYQSRSEFL 1569  
 QY 242 ---NSVSELKIPCKNPLFTGGSAS-----ATLTGLD-----SPCSDQMVLRAL 284  
 Db 1570 DVNVLILANSVKNGSPESQYTKTAQIVNVVQYTLTEYDEHITOLEKDICTAKEALEB- 1628  
 QY 285 LSQLTQID----GSLGPKESQSGESSESLLTIDGI 317  
 Db 1629 -AEESLDPMTPGYPYTPQPDLYDTNTSLSMSRDASV 1664

RESULT 2  
 ID IRAL\_YEAST  
 AC IRAL\_YEAST STANDARD; PRT; 3092 AA.  
 ID P18963;  
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibitory regulator protein IRAL.  
 GN IRAL OR PPD1 OR GLC1 OR YBR140C OR YBR1016.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE OF 1-2767 FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=95274325; PubMed=7754712;  
 RA Zagulski M., Becam A.-M., Grzybowska E., Lacroute F., Migdalski A.,  
 RA Slonimski P.P., Sokolowska B., Herbert C.J.;  
 RT "The sequence of 12.5 kb from the right arm of chromosome II predicts  
 RT a new N-terminal sequence for the IRAL protein and reveals two new  
 RT genes, one of which is a DEAD-box helicase.";  
 RL Yeast 10:1227-1234 (1994).  
 RN [2]  
 RP SEQUENCE OF 155-3092 FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=89219070; PubMed=2540426;  
 RA Tanaka K., Matsumoto K., Toh-E A.;  
 RT "IRAL, an inhibitory regulator of the RAS-cyclic AMP pathway in  
 RT Saccharomyces cerevisiae.";  
 RL Mol. Cell. Biol. 9:757-768 (1989).  
 RN [3]  
 RP SEQUENCE OF 2768-3092 FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=94378717; PubMed=8091856;  
 RA Becam A.-M., Cullin C., Grzybowska E., Lacroute F., Nasr F.,  
 RA Oztier-Kalogeropoulos O., Palucha A., Slonimski P.P., Zagulski M.,  
 RA Herbert C.J.;  
 RT "The sequence of 29.7 kb from the right arm of chromosome II reveals  
 RT 13 complete open reading frames, of which ten correspond to new  
 RT genes.";  
 RL Yeast 10:SL-S11 (1994).  
 CC -!- FUNCTION: INHIBITORY REGULATOR OF THE RAS-CYCLIC AMP  
 CC PATHWAY IN SACCHAROMYCES CEREVISIAE. STIMULATES THE GTPASE  
 CC ACTIVITY OF RAS PROTEINS.  
 CC -!- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL; M24378; AAA34709.1; -;  
 CC EMBL; X75891; CAA53498.1; -;  
 CC EMBL; Z36009; CAA85098.1; -;  
 CC EMBL; X78937; CAA55537.1; -;  
 CC PIR; S46009; S46009.  
 CC SGD; S0000344; IRAL.  
 CC InterPro; IPR001936; RasGAP.  
 CC Pfam; PF00616; RasGAP; 1.  
 CC SMART; SM00323; RasGAP; 1.  
 CC PROSITE; PS00509; RAS\_GTPASE\_ACTIV\_1; 1.  
 CC PROSITE; PS50018; RAS\_GTPASE\_ACTIV\_2; 1.  
 CC GTPase activation; Phosphorylation.  
 KW DOMAIN 1709 1898 RAS-GAP.  
 FT DOMAIN 326 331 POLY-SER.  
 FT DOMAIN 379 383 POLY-SER.  
 FT DOMAIN 475 484 POLY-ASN.  
 FT DOMAIN 1433 1437 POLY-ILE.  
 FT DOMAIN 2039 2042 POLY-GLU.  
 FT MOD\_RES 1753 1753 PHOSPHORYLATION (BY CAPK)  
 FT MOD\_RES 3004 3004 (POTENTIAL).  
 FT MOD\_RES 361 361 PHOSPHORYLATION (BY CAPK)  
 FT MOD\_RES 361 361 (POTENTIAL).  
 FT CONFLICT 361 361 V -> G (IN REF. 2).  
 FT SEQUENCE 3092 AA; 350974 MW; 291339AESBD26E08 CRC64;



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CC DR EMBL; L04284; AAS58669.1; -  
 CC DR EMBL; 269744; CAA93625.1; -  
 CC DR EMBL; 269745; CAA93625.1; JOINED.  
 CC DR EMBL; 269746; CAA93625.1; JOINED.  
 CC DR EMBL; 269747; CAA93625.1; JOINED.  
 CC DR EMBL; 269748; CAA93625.1; JOINED.  
 CC DR EMBL; 269749; CAA93625.1; JOINED.  
 CC DR EMBL; 269750; CAA93625.1; JOINED.  
 CC DR EMBL; 269751; CAA93625.1; JOINED.  
 CC DR EMBL; 269752; CAA93625.1; JOINED.  
 CC DR EMBL; 269753; CAA93625.1; JOINED.  
 CC DR EMBL; 269754; CAA93625.1; JOINED.  
 CC DR EMBL; 269755; CAA93625.1; JOINED.  
 CC DR EMBL; 269756; CAA93625.1; JOINED.  
 CC DR EMBL; 269757; CAA93625.1; JOINED.  
 CC DR EMBL; 269758; CAA93625.1; JOINED.  
 CC DR EMBL; 269759; CAA93625.1; JOINED.  
 CC DR EMBL; 269760; CAA93625.1; JOINED.  
 CC DR EMBL; 269761; CAA93625.1; JOINED.  
 CC DR EMBL; 269762; CAA93625.1; JOINED.  
 CC DR EMBL; 269763; CAA93625.1; JOINED.  
 CC DR EMBL; 269764; CAA93625.1; JOINED.  
 CC DR EMBL; 269765; CAA93625.1; JOINED.  
 CC DR EMBL; 269766; CAA93625.1; JOINED.  
 CC DR EMBL; 269767; CAA93625.1; JOINED.  
 CC DR EMBL; 269768; CAA93625.1; JOINED.  
 CC DR EMBL; 269769; CAA93625.1; JOINED.  
 CC DR EMBL; 269770; CAA93625.1; JOINED.  
 CC DR EMBL; 269772; CAA93625.1; JOINED.  
 CC DR EMBL; 269773; CAA93625.1; JOINED.  
 CC DR EMBL; 269774; CAA93625.1; JOINED.  
 CC DR EMBL; 269775; CAA93625.1; JOINED.  
 CC DR EMBL; 269776; CAA93625.1; JOINED.  
 CC DR EMBL; 269777; CAA93625.1; JOINED.  
 CC DR EMBL; 269778; CAA93625.1; JOINED.  
 CC DR EMBL; 269779; CAA93625.1; JOINED.  
 CC DR EMBL; 269780; CAA93625.1; JOINED.  
 CC DR EMBL; D14540; BAA03407.1; -  
 CC DR EMBL; L01986; AAA92511.1; -  
 CC DR EMBL; U04737; AAA18644.1; -  
 CC DR EMBL; S78570; AAB34770.1; -  
 CC DR EMBL; X81604; CAA58584.1; -  
 CC DR EMBL; S66432; AAB28545.1; -  
 CC DR EMBL; AF231998; AAG26332.2; ALT\_TERM.  
 CC DR TRANSFAC; T02337; -  
 CC DR MIM; 159555; -  
 CC DR InterPro; IPR001487; Bromodomain.  
 CC DR InterPro; IPR003889; FYrich.C.  
 CC DR InterPro; IPR003888; FYrich.N.  
 CC DR InterPro; IPR001965; PHD.  
 CC DR InterPro; IPR003616; PostSET.  
 CC DR InterPro; IPR001214; SET.  
 CC DR InterPro; IPR002857; Znf-CXXC.  
 CC DR Pfam; PF00628; PHD; 3.  
 CC DR Pfam; PF00856; SET; 1.  
 CC DR Pfam; PF02008; zf-CXXC; 1.  
 CC DR SMART; SM00297; BROMO; 1.  
 CC DR SMART; SM00542; FYRC; 1.  
 CC DR SMART; SM00541; FYRN; 1.  
 CC DR SMART; SM00249; PHD; 4.  
 CC DR SMART; SM00508; PostSET; 1.  
 CC DR SMART; SM00317; SET; 1.  
 CC DR PROSITE; PS00014; BROMODOMAIN\_2; 1.  
 CC DR PROSITE; PS0280; SET; 1.  
 CC KW Proto-oncogene; Chromosomal translocation; DNA-binding; Bromodomain;  
 CC KW Nuclear protein; Zinc-finger; Metal-binding; Transcription regulation;  
 CC KW Alternative splicing.

FT DOMAIN 17 102 ALA/GLY/SER-RICH.  
 FT DNA\_BIND 169 180 A.T HOOK (BY SIMILARITY).  
 FT DNA\_BIND 217 227 A.T HOOK (BY SIMILARITY).  
 FT DNA\_BIND 301 309 A.T HOOK (BY SIMILARITY).  
 FT ZN\_FING 1147 1194 CXXC-TYPE.  
 FT ZN\_FING 1431 1482 PHD-TYPE 1.  
 FT ZN\_FING 1484 1533 PHD-TYPE 2.  
 FT ZN\_FING 1566 1627 PHD-TYPE 3.  
 FT DOMAIN 1703 1748 BROMODOMAIN (DIVERGENT).  
 FT DOMAIN 3840 3969 SET.  
 FT DOMAIN 137 143 POLY-GLY.  
 FT DOMAIN 561 564 POLY-PRO.  
 FT DOMAIN 568 571 POLY-PRO.  
 FT SITE 1362 1363 BREAKPOINT FOR TRANSLOCATION TO FORM MLL-  
 Query Match 5.4%; Score 95; DB 1; Length 3969;  
 Best Local Similarity 21.1%; Pred. No. 10;  
 Matches 68; Conservative 39; Mismatches 124; Indels 92; Gaps 13;  
 QY 38 MRRSLNNHRRPPLVLIQV-----DLNKEPMDIPKMACYGGKDWYFYSDRDK 85  
 DB 2006 LRRKFLNGLEPENIHMMIGSMTIDCLGILNLDSDCE-----DKL 2044  
 QY 86 YATGLTNRATATGYKATGKDRITLIRKGLVGRKTLVFGYGRAPRGRKTDVWHEFRL 145  
 DB 2045 FPIGYQCSRV-----YWTTDARKRCVYTKIVECRPPV-----EPDINST--VEHDENR 2093  
 QY 146 QGSHPPNHSLSPEKDWLRCVFKHNTGVC-----RDNMGSCFETASASLPP 196  
 DB 2094 TIAHSPTSFTESSSKES-----QNTAEIISPPSPDRPHSQTSGCYHYHVIS-KVPR 2144  
 QY 197 LMDP-YINFDOEP-----SSYLSDDHHVILNEHVPCFNSLQNTLNSLNTNSYSELK 248  
 DB 2145 IRTFSYPTQRSGCRLPPLSAGSPTTTHIVTVGDPLLSGLRSIGSRHRHSSTSSLPQR 2204  
 QY 249 IPCKNPPLFTGG-----SASATLTGLDSFCSDDQMLRAL-----LSQLTKIDG 293  
 DB 2205 SKLIMSPMRGTNTYRNNTYSSVSTTGTATDLESSAKVVDHVLGPLNSSLTSLQNTSTSS 2264  
 QY 294 SL-----GPKESQSYGEGSSSE 309  
 DB 2265 NLQRTVTVTVGNKSHLDGSSSE 2287  
 RESULT 4  
 Y009\_HUMAN STANDARD; PRT; 314 AA.  
 ID Y009\_HUMAN  
 AC Q15390;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein KIAA0009.  
 GN KIAA0009.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=96051387; PubMed=7584026;  
 RA Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,  
 RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;  
 RT "Prediction of the coding sequences of unidentified human genes. I.  
 RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
 RT analysis of randomly sampled cDNA clones from human immature myeloid  
 RT cell line KG-1.";  
 RL DNA Res. 1:27-35(1994).  
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## RESULT 6

HRX\_MOUSE STANDARD; PRT; 3866 AA.

AC P55200;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Zinc finger protein HRX (ALL-1) (Fragment).

GN MLL OR HRX OR ALL1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN=C57BL/6J, AND B6/CBA; TISSUE=Spleen, and Lung;

RA MEDLINE=93317679; PubMed=8327517;

RA Ma Q., Alder H., Nelson K.K., Chatterjee D., Gu Y., Nakamura T.,

RA Canaani E., Croce C.M., Siracusa L.D., Buchberg A.M.;

RT "Analysis of the murine All-1 gene reveals conserved domains with

RT human ALL-1 and identifies a motif shared with DNA

RT methyltransferases.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:6350-6354(1993).

CC -!- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.

CC MAY REGULATE GENES INVOLVED IN SKELETAL FORMATION DURING

CC EMBRYONIC DEVELOPMENT.

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -!- SIMILARITY: BELONGS TO THE TRANSCRIPTION FACTOR TRITHORAX FAMILY.

CC -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.

CC -!- SIMILARITY: CONTAINS 1 SET DOMAIN.

CC -!- SIMILARITY: CONTAINS 3 PHD-TYPE ZINC FINGERS.

CC -!- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.

CC -----

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CC -----

DR EMBL; LI7069; AA62593.1; -

DR MGD; MGI:96995; M1.

DR InterPro: IPR001487; Bromodomain.

DR InterPro: IPR003889; FYrich\_C.

DR InterPro: IPR003888; FYrich\_N.

DR InterPro: IPR001965; PHD.

DR InterPro: IPR003616; PostSET.

DR InterPro: IPR000093; Recf.

DR InterPro: IPR001214; SET.

DR InterPro: IPR002857; znf-CXXC.

DR Pfam; PF00628; PHD; 3.

DR Pfam; PF00856; SET; 1.

DR Pfam; PF02008; zf-CXXC; 1.

DR SMART; SM00297; BROMO; 1.

DR SMART; SM00542; FYRC; 1.

DR SMART; SM00541; FYRN; 1.

DR SMART; SM00249; PHD; 4.

DR SMART; SM00508; PostSET; 1.

DR SMART; SM00317; SET; 1.

DR PROSITE; PS50014; BROMODOMAIN\_2; 1.

DR PROSITE; PS50280; SET; 1.

KW DNA-binding; Nuclear protein; Zinc-finger; Metal-binding;

KW Transcription regulation; Alternative splicing; Polymorphism.

FT NON\_TER 1 1

FT DNA\_BIND 67 78 A-T HOOK (BY SIMILARITY).

FT DNA\_BIND 115 125 A-T HOOK (BY SIMILARITY).

FT DNA\_BIND 199 207 A-T HOOK (BY SIMILARITY).

FT ZN\_FING 1044 1091 CXXC-TYPE.

FT ZN\_FING 1330 1381 PHD-TYPE 1.

FT ZN\_FING 1383 1432 PHD-TYPE 2.

FT ZN\_FING 1465 1529 PHD-TYPE 3.

FT DOMAIN 1605 1650 BROMODOMAIN (DIVERGENT).

FT DOMAIN 3737 3846 SET.

FT DOMAIN 35 41 POLY-GLY.

FT DOMAIN 459 469 PRO-RICH.

FT DOMAIN 1231 1238 POLY-PRO.

FT DOMAIN 3533 3536 POLY-GLU.

FT DOMAIN 3693 3697 POLY-GLU.

FT VARSPLIC 1503 1505 MISSING (IN ISOFORM 2).

FT VARIANT 1497 1497 K -> T.

SO SEQUENCE 3866 AA; 420976 MW; ADFC55E14E806FID CRC64;

Query Match 5.0%; Score 87.5; DB 1; Length 3866;

Best Local Similarity 19.5%; Pred. No. 46;

Matches 63; Conservative 43; Mismatches 140; Indels 77; Gaps 11;

QY 38 MRRSLHNNRPLVLIQV-----DLNKCEPMDIPKMACVGGKQWYFYSDRDK 85

Db 1908 LRRKFLNGLEPENIHMMIGMTIDCLGLNLSDC-----DKL 1946

QY 86 YATGLRTNRATATGYKATGKDRILRKGLVGRKTLVFYQGRAPRKTDWMHEERL 145

Db 1947 FPIGTQSRV---YWTDDARKRCVYTKIMECPVW-----EPDINST--VEHDDNR 1995

QY 146 QGSHPPNHSLSPEKEDWVLCRVF-----HKNTGEVICRDMNGSCFDETSASLPL 197

Db 1996 TIAHSPSFIDASCCKDSQSTAAILSPSPDRPHSOTS-----GSCYHVVIS-KVPRI 2046

QY 198 MDP-YINFDEP-----SSYLSDDHHYIINEHVPCFNSLSONQTLNSLTSVSELKI 249

Db 2047 RTPSYSPQTRSPGCRPLPSAGSPPTTHEIVTGDPLLSGLRSIGRRHSTSLSPRS 2106

QY 250 PCKNPPLFTGGSASATL-----TGLDSFCSDDQVLFALISQLTKIDGSLGPKESQ 301

Db 2107 KLRI MSPVTSAYSRSSVSPSLGTATDEASAKADRGLLSSANLGHSAAPPSSS 2166

QY 302 SYGEGSSSLTDIGIPSTVWNC 324

Db 2167 QRTVGSKTSHLDGSSPSEVKRC 2189

## RESULT 7

CID\_DROME

ID CID\_DROME STANDARD; PRT; 1377 AA.

AC P19538;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Cubitus interruptus dominant protein.

GN CI-D.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OREGON-R;

RX MEDLINE=90346286; PubMed=2166702;

RA Orenic T.V., Slusarski D.C., Kroell K.L., Holmgren R.A.;

RT "Cloning and characterization of the segment polarity gene cubitus

RT interruptus dominant of Drosophila.";

RL Genes Dev. 4:1053-1067(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=OREGON-R;

RX MEDLINE=92146935; PubMed=1686006;

RA Berry A.J., Ajioka J.W., Kreilman M.;

RT "Lack of polymorphism on the Drosophila fourth chromosome resulting

RT from selection.";







```
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable nicotinate phosphoribosyltransferase (EC 2.4.2.11)
DE (NAPRTase).
GN NP1 OR YOR209C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=FL100;
RA Lalo D., Dolra C., Thuriaux P.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Hughes B., Pohl T.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 1-43 FROM N.A.
RC STRAIN=FL100;
RX MEDLINE=93296170; PubMed=8516295;
RA Lalo D., Carles C., Sentenac A., Thuriaux P.;
RT "Interactions between three common subunits of yeast RNA polymerases
RT I and III.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5524-5528(1993).
CC -!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
CC nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -!- PATHWAY: FIRST STEP IN PREISS-HANDLER PATHWAY LEADING TO THE
CC SYNTHESIS OF NAD.
CC -!- SIMILARITY: BELONGS TO THE NAPRTASE FAMILY.
CC -----
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CC -----
DR EMBL; Z36878; CAA85352.1; -
DR EMBL; Z75117; CAA99424.1; -
DR EMBL; L11274; AAB59317.1; -
DR PIR; S48884; S48884.
DR SGD; S0005735; NP11.
DR CONFLICT 131 137 YEIPLLS -> MRLSTV (IN REF. 1).
DR CONFLICT 144 159 FKEVDIDWDYENQLEQ -> LIYTSGLNRHQ (IN
DR REF. 1).
DR CONFLICT 175 177 SEF -> RIH (IN REF. 1).
DR CONFLICT 243 243 E -> EL (IN REF. 1).
DR SEQUENCE 429 AA; 49018 MW; F3F7941476C3398B CRC64;

Query Match 4.8%; Score 84.5; DB 1; Length 429;
Best Local Similarity 18.4%; Pred. No. 4.3;
Matches 72; Conservative 56; Mismatches 140; Indels 123; Gaps 21;

QY 3 TEEMKESISWVEAKLP-----PGRFHPKDD-ELVCDVLMRSLNNHRPP 49
DB 66 TEEE-----EYLQKEIPLPSAIVIKYISSNKLHPHEQISFTSEIEGKPHYKLK-- 118
QY 50 LVLIQVDLNKCEPNDIPKACVGGK-----DWFY---YSQRDKYAT----- 88
DB 119 -ILVSGSWKOTILVEIPLLSLSAYFKFVDIDWDYENQLEQAEKKAETLFDNGIRSEF 177
QY 89 GLRNRATAT-----GYWAT--GKDRITLRGKLVGMKTLVFFQ--GRAPGRKT-DW 138
DB 178 GTRRRSLKAQDLIMQGIKAVNGNPDR---NKSLLGTSNILLFAKKYGVKPGTVAHEW 234
QY 139 VMHEFRLOGSHHPNHSPPKEDWLCRVFHNKTEGICRDNMGSCFDETSASLPPLM 198
DB 235 VMGVASISDY---LHANKNAMDCWI---NTEGAKNAGLALTDFTGT--DDFLKSRFPYS 287
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QY 199 DPVINFQD---EPSSYLS-DHHYIINEHVPCFSN-LSQNTLN----- 237
DB 288 DAVGVGVQSDGDPVEYTKKISHHYHDVLKLPKFSKIICYSDSLNVEKAITYSAAKENG 347
QY 238 -----SNLTSVSELKIPCKNPNPLFTGGASATLTGLDSCSDQMVLRALLSQT 290
DB 348 LATFGTGTNTNDFRKKSEPOVKSEPL-----NIVIKLIE 382
QY 291 IGSGLGPKESQSYGEGSSESLTLDIGIPSTV 321
DB 383 VGNHAIKISDNLGK-----NMGDPAIV 405

RESULT 11
HAIR_MOUSE
ID HAIR_MOUSE STANDARD; PRT; 1182 AA.
AC Q61645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hairless protein.
GN HR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SKIN;
RX MEDLINE=94329587; PubMed=8052649;
RA Cachon-Gonzalez M.B., Fenner S., Coffin J.M., Moran C., Best S.,
RA Stoye J.P.;
RT "Structure and expression of the hairless gene of mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).
CC -!- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, HAIR
CC FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION IN
CC DERMIS.
CC -!- DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
CC INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR
CC FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH
CC CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER
CC MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED
CC RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOZYGOUS FOR
CC HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED
CC SKIN TUMORS.
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CC -----
DR EMBL; Z32675; CAA83587.1; -
DR MGD; MGI:96223; hr.
DR InterPro; IPR003347; JmJC.
DR Pfam; PF02373; JmJC; 1.
KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
KW Metal-binding.
FT ZN-FING 595 620 C6-TYPE.
FT DOMAIN 535 540 POLY-GLY.
FT SEQUENCE 1182 AA; 127182 MW; EFB0EE62AE81B40 CRC64;

Query Match 4.8%; Score 84.5; DB 1; Length 1182;
Best Local Similarity 23.0%; Pred. No. 17;
Matches 59; Conservative 16; Mismatches 92; Indels 89; Gaps 11;
```



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OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RL NCBI_TaxID=4896;
CC -!- SIMILARITY: SOME, TO YEAST YKLI08W.
CC
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CC
CC EMBL; Z98531; CAB11071.1; -.
CC DOMAIN 224 232 POLY-SER
CC SEQUENCE 337 AA; 38684 MW; 30A532A8C63222B1C CRC64;
CC
Query Match 4.8%; Score 83.5; DB 1; Length 337;
Best Local Similarity 23.3%; Pred. No. 3.8;
Matches 49; Conservative 25; Mismatches 75; Indels 61; Gaps 9;
QY 135 KTDVWHEFRFLOSHPPNHSLSPPKEDWVLCRVFKHKEGVICRDNMGSCDFEASASL 194
DB 67 KVDFKFTPTKQRAETEANESKPRNDYL--QVTPKT-----DKSLLGPT 111
QY 195 PPLMDYVINDQBPSSVLSDDHYIINEHVPCFNSLSQNTLSNVTNSVSELKI---PC 251
DB 112 POLSRRVLN-----LLEDMPADSHVDQISDKHN-----TSELSMTMPTTFS 156
QY 252 KNPPLFTGGSASATLTGLDSFGSSQDWV-----LRALLSQLTKIDGSL 295
DB 157 KNPFPV-----AQHTPTVLETPSSRYLQVYTPNLLRVNAPCRKLSLEMLRELKIDEDDY 211
QY 296 KNPES-----QSYGGSSSLL--TDGIP 318
DB 212 GSNEKILQEFESFSSSSSLVDRLDISQ 241
RESULT 14
ID IF37_ARATH STANDARD; PRT; 591 AA.
AC P56820;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative eukaryotic translation initiation factor 3 subunit 7 (eIF-3
DE zeta).
GN A74G20980 OR T13K14.140.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Griveill L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delzeny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Bontroy M., Bancroft I.,
RA Vos P., Honelisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

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RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Iankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,
RA Pettitt A., Rajandream M.A., Lyne M., Benes V., Lechmann T.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Roehmann T.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,
RA Neumann S., Agrion A., Vitale D., Liguori R., Piravandi E.,
RA Massenat O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Jochu C.,
RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana";
RL Nature 402:769-777(1999).
CC -!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
CC METHIONYL-TRNAI AND MRNA. ASSOCIATES WITH THE SUBUNIT P170 OF
CC EIF3 (BY SIMILARITY).
CC -!- SURUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS (BY
CC SIMILARITY)
CC -!- SIMILARITY: BELONGS TO THE EIF3S7 FAMILY.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL080282; CAB45893.1; -.
CC EMBL; AL161554; CAB79098.1; -.
KW Hypothetical protein; Initiation factor; Protein biosynthesis.
SQ SEQUENCE 591 AA; 66724 MW; 9C5E673F04E9845C CRC64;
Query Match 4.8%; Score 83.5; DB 1; Length 591;
Best Local Similarity 19.6%; Pred. No. 8.2;
Matches 75; Conservative 44; Mismatches 122; Indels 141; Gaps 18;
QY 8 KESSISMVEAKLPPGFRPHK-----DDELVC-----DYLRRSLHN 44
DB 106 EDAAFLVKGKPPPRKFGKWRPNHNNLPQRDEEVEAKKRDKAEKARDRLYN 165
QY 45 NHRPPL-----VLQVDLNC-----EPWDIPKMACVCGKD 75
DB 166 NNRRNIHRRREAAAFKSSVDIQENWMLQIPFTFSKLSVTQVEPDL--LLC-GGLE 222
QY 76 WY-----EVSORDRYATGLRTNATATGYWKGATGKRTILRKGLKGMKRTLVFYQGR 129
DB 223 YNNRFRDRTTPKNER-----RLERKRNFFKVTSSDDPVIR--FLAKEDKATVFATDA 274

```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:57:08 ; Search time 29.23 seconds  
(without alignments)

1917.563 Million cell updates/sec

Title: US-09-889-926-2

Perfect score: 1757

Sequence: 1 METEEMKESSISWEAKLP.....EGSSESLITDIPSTVWNC 324

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_l9.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1757	100.0	324	10	Q9SE10	Q9se10 arabidopsis
2	1579.5	89.9	309	10	Q9SGS9	Q9sgs9 arabidopsis
3	967	56.2	279	10	Q9LS11	Q9ls11 arabidopsis
4	946	53.8	299	10	Q93XA7	Q93xa7 phaseolus v
5	557	31.7	329	10	Q9FLR3	Q9flr3 arabidopsis
6	552.5	31.4	327	10	Q40880	Q40880 petunia hyb
7	548	31.2	336	10	Q9FLJ2	Q9flj2 arabidopsis
8	545.5	31.0	335	10	Q9FK44	Q9fk44 arabidopsis
9	544	31.0	375	10	Q04017	Q04017 arabidopsis
10	542	30.8	331	10	Q9SC68	Q9sc68 oryza sativ
11	542	30.8	331	10	Q9SM90	Q9sm90 oryza sativ
12	536.5	30.5	334	10	Q9S851	Q9s851 arabidopsis
13	535.5	30.5	314	10	Q9LS50	Q9ls50 arabidopsis
14	533	30.3	318	10	Q9LJW3	Q9ljw3 arabidopsis
15	532.5	30.3	338	10	Q9SQQ6	Q9sqq6 arabidopsis
16	519	29.5	285	10	Q9FKA0	Q9fka0 arabidopsis

17	517	29.4	324	10	Q9AV06	Q9av06 oryza sativ
18	512	29.1	310	10	Q9FRV4	Q9frv4 arabidopsis
19	512	29.1	337	10	Q9LIL8	Q9lil8 arabidopsis
20	505.5	28.8	316	10	Q9ZQ25	Q9zq25 arabidopsis
21	500	28.5	320	10	Q9FTY0	Q9fty0 oryza sativ
22	491.5	28.0	365	10	Q9SL41	Q9sl41 arabidopsis
23	477	27.1	351	10	Q9ZR22	Q9zr22 triticum sp
24	473	26.9	298	10	Q9SLK1	Q9slk1 arabidopsis
25	472.5	26.9	334	10	Q9M274	Q9m274 arabidopsis
26	470.5	26.8	324	10	Q9C8W9	Q9c8w9 arabidopsis
27	466	26.5	256	10	Q93XA6	Q93xa6 phaseolus v
28	461	26.2	317	10	Q9LDY8	Q9ldy8 arabidopsis
29	459.5	26.2	399	10	Q9L033	Q9l033 arabidopsis
30	458.5	26.1	418	10	Q9SI80	Q9si80 arabidopsis
31	458	26.1	316	10	Q9MBC6	Q9mbc6 oryza sativ
32	456.5	26.0	348	10	Q9LVA1	Q9lva1 arabidopsis
33	456	26.0	377	10	Q65508	Q65508 arabidopsis
34	456	26.0	418	10	Q9ZVH0	Q9zvho arabidopsis
35	453.5	25.8	631	10	Q9SRZ8	Q9srz8 arabidopsis
36	452.5	25.8	297	10	Q93VY3	Q93vy3 arabidopsis
37	449.5	25.6	395	10	Q9SNM6	Q9snm6 oryza sativ
38	446.5	25.4	341	10	Q9SV87	Q9sv87 arabidopsis
39	446.5	25.4	349	10	Q9SOL0	Q9sol0 lycopersico
40	444	25.3	337	10	Q9FIW5	Q9fiw5 arabidopsis
41	442	25.2	246	10	Q9LSH5	Q9lsh5 arabidopsis
42	439.5	25.0	301	10	Q948Z2	Q948z2 solanum tub
43	439	25.0	320	10	Q9ZNU2	Q9znu2 arabidopsis
44	438.5	25.0	358	10	Q9LP17	Q9lp17 arabidopsis
45	437.5	24.9	476	10	Q9FFI5	Q9ffi5 arabidopsis

#### ALIGNMENTS

RESULT 1

ID	Q9SE10	PRELIMINARY;	PRT;	324 AA.
AC	Q9SE10;			
DC	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	NAC1 (F14JL6.32).			
GN	NAC1.			
OS	Arabidopsis thaliana (Mouse-ear cross).			
OC	Eukaryota; Viridiplantae; Streptophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=CV. LANDSBERG;			
RA	Xie Q., Chua N.H.;			
RT	"Arabidopsis NAC1 transduces auxin signal to promote later root development";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RA	SEQUENCE FROM N.A.			
RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;			
RT	"Genomic sequence for Arabidopsis thaliana BAC F14JL6 from chromosome I.,"			
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RA	SEQUENCE FROM N.A.			
RA	Ecker J.R.;			
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RA	SEQUENCE FROM N.A.			

RA Ecker J.R.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altai H., Bel B., Chin C., Chiou J., Choi E.,  
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howling B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF198054; AAF21437.1; -;  
 DR EMBL; AC002304; AAF79328.1; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 324 AA; 36569 MW; C70ED705D1A66957 CRC64;

Query Match 100.0%; Score 1757; DB 10; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-161;  
 Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METEEMKESISWVEAKLPDGFPHKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 Db 1 METEEMKESISWVEAKLPDGFPHKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 QY 61 EPWDIPKMACVGGKDWYFYSDRDKYATGLRTNRTATGYWKATGKDRITLKGK 120  
 Db 61 EPWDIPKMACVGGKDWYFYSDRDKYATGLRTNRTATGYWKATGKDRITLKGK 120  
 QY 121 KTLVYQGRAPGRKTDWYMHFRLOGSHHPNHLSSPKEDWVLCRVFHKNTGVC 180  
 Db 121 KTLVYQGRAPGRKTDWYMHFRLOGSHHPNHLSSPKEDWVLCRVFHKNTGVC 180  
 QY 181 NMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 240  
 Db 181 NMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 240  
 QY 241 TNSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQWVLRALLSQTIDGSLGPKES 300  
 Db 241 TNSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQWVLRALLSQTIDGSLGPKES 300  
 QY 301 QSYGEGSSSESLTLDIGIPSTVWNC 324  
 Db 301 QSYGEGSSSESLTLDIGIPSTVWNC 324

RESULT 2  
 Q9SGS9 PRELIMINARY; PRT; 309 AA.  
 ID Q9SGS9  
 AC Q9SGS9;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE T6H22.19 PROTEIN.  
 GN T6H22.19.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Altafi H., Nguyen M., Lam B., Buehler E., Dunn P., Gonzalez A.,  
 RA Kremenetskaia I., Kim C., Lenz C., Li J., Liu S., Luross S.,  
 RA Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AC009894; AAF02847.1; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 309 AA; 34715 MW; 2A263CD213E44688 CRC64;

Query Match 89.9%; Score 1579.5; DB 10; Length 309;  
 Best Local Similarity 91.8%; Pred. No. 7.8e-144;  
 Matches 302; Conservative 0; Mismatches 2; Indels 25; Gaps 3;

QY 1 METEEMKESISWVEAKLPDGFPHKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 Db 1 METEEMKESISWVEAKLPDGFPHKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 QY 61 EPWDIP-----KMACVGGKDWYFYSDRDKYATGLRTNRTATGYWKATGKDRITLKGK 115  
 Db 61 EPWDIPMYNTTKRVCV-----QDRKYATGLRTNRTATGYWKATGKDRITLKGK 111  
 QY 116 LVGMKTLVYQGRAPGRKTDWYMHFRLOGSHHPNHLSSPKEDWVLCRVFHKNTG 175  
 Db 116 LVGMKTLVYQGRAPGRKTDWYMHFRLOGSHHPNHLSSPKEDWVLCRVFHKNTG 175  
 QY 176 VICRDNMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 235  
 Db 161 VICRDNMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 220  
 QY 236 LNSLNTSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQWVLRALLSQTIDGSL 295  
 Db 221 LNSLNTSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQWVLRALLSQTIDGSL 280  
 QY 296 GPKESQSYGEGSSSESLTLDIGIPSTVWNC 324  
 Db 281 GPKESQSYGEGSSSESLTLDIGIPSTVWNC 309

RESULT 3  
 Q9LS11 PRELIMINARY; PRT; 279 AA.  
 ID Q9LS11  
 AC Q9LS11;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE NAM (NO APICAL MERISTEM) PROTEIN-LIKE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC  
 RT clones";  
 RL DNA Res. 7:131-135(2000).  
 DR EMBL; AB026645; BAB02506.1; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 279 AA; 31946 MW; 376EE552927C416 CRC64;



Query Match 56.2%; Score 987; DB 10; Length 279;  
 Best Local Similarity 62.0%; Pred. No. 7.5e-87;  
 Matches 203; Conservative 24; Mismatches 46; Indels 50; Gaps 9;

QY 4 EEEMKESSISWVEAKLPGRFHPKDDLVCDYLMRSLHNHRPPLVLIQVDLNKCEPW 63  
 Db 3 ETEKNKGSISWVEANLPPGRFHPKDDLVCDYLMRSLHNHRPPLVLIQVDLNKCEPW 61  
 QY 64 DIPKMACVGGKDWYFYQSQRDKYATGLRTNRATATGYWKATGKDRITILRKGLVGMKRKL 123  
 Db 62 DIPOTARVGGKEWYFYQSQRDKYATGYRTNRATATGYWKATGKDRATQRNGGLVGMKRKL 121  
 QY 124 VFYQGRAPGRKTDWVHFEFLQGS--HHPPNHSLSPPKEDVLCRVFHKNTGCVICRDN 181  
 Db 122 VFYGRSPGRKTDWVHFEFLQGLLHSPN----SLEEWVLCRVFHKNSGADIDDI 177  
 QY 182 MGSCFDEATASLPLMDPYNFDEPSSYSDHHYIINEHVPCFS-NLSQNOTNSNL 240  
 Db 178 TRSCSDATASA---FMDSYNF-----DHHIILNHQVPCFSNLSHNTQNSGL 223  
 QY 241 TNSVSELKIPCKNPPLFTGGSSASATLTGLDFSCSSDQWVLRALLSQTAKIDGSLGPKES 300  
 Db 224 IS-----KNSSPLFN-----ASPDQMILRTLLSQTAK-----KVEES 255  
 QY 301 QSYGGSSESILTDIGIPSTVWN 323  
 Db 256 QSRGDGSESQLTLDIGIPSHAWN 278

RESULT 4  
 Q93XA7 PRELIMINARY; PRT; 299 AA.  
 ID Q93XA7  
 AC Q93XA7  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE NAC DOMAIN PROTEIN NACL  
 OS Phaseolus vulgaris (kidney bean) (French bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 OX NCBI\_TaxID=3885;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. RED KIDNEY; TISSUE=LEAF ABCISSION ZONE;  
 RA Whitelaw C.A., Lyssenko N.G., Thal V.K., Nath P., Tucker M.L.;  
 RT "Functional analysis of regulatory elements in the gene promoter for  
 RT an abscission-specific cellulase from bean (Phaseolus vulgaris) and  
 RT characterization of candidate transcription factors";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF402602; AAK84883.1; -  
 DR SEQUENCE 299 AA; 33877 MW; 028D011BE405327D CRC64;  
 SQ SEQUENCE 299 AA; 33877 MW; 028D011BE405327D CRC64;

Query Match 53.8%; Score 946; DB 10; Length 299;  
 Best Local Similarity 60.2%; Pred. No. 7.3e-83;  
 Matches 192; Conservative 44; Mismatches 55; Indels 28; Gaps 9;

QY 10 SSSISWVEAKLPGRFHPKDDLVCDYLMRSLHNHRPPLVLIQVDLNKCEPMDIPKMA 69  
 Db 2 SNISWVEAKLPGRFHPKDDLVCDYLMRSLHNHRPPLVLIQVDLNKCEPMDIPKMA 58  
 QY 70 CVGSKDWYFYQSQRDKYATGLRTNRATATGYWKATGKDRITILRKGLVGMKRKLTVYQGR 129  
 Db 59 CVGSKDWYFYQSQRDKYATGLRTNRATATGYWKATGKDRITILRKGLVGMKRKLTVYQGR 118  
 QY 130 APRGRKTDWVHFEFLQGS--HHPPNHSLSPPKEDVLCRVFHKNTGCVICRDNMGSCFDET 189  
 Db 119 APRGRKTDWVHFEFLQGS--HHPPNHSLSPPKEDVLCRVFHKNTGCVICRDNMGSCFDET 175  
 QY 190 ASASLPLMDPYNFDEPSSYSDHHYIINEHVPCFSNLSQNT--LNSNLTNVSEL 247  
 Db 176 GSSSLPALMDSYISFDTQTA-----HADEFQVPCFSIFSONQANPFIHMTTMEPKL 228

QY 248 KIPCKNPPLFTGGSSASATLTGLDFSCSSDQWVLRALLSQTAKIDG--SLGPKESQSYG 304  
 Db 229 -----PATTYGGAPNLGYCLDPL-SCDRKVLKAVLSQITKMERPNLQSLGKSTSG 279  
 QY 305 EGSSSESLTDIGIPSTVWN 323  
 Db 280 EGSSSESLYSEVGMGP-MWN 297

RESULT 5  
 Q9FLR3 PRELIMINARY; PRT; 329 AA.  
 ID Q9FLR3  
 AC Q9FLR3  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE NAM (NO APICAL MERISTEM)-LIKE PROTEIN.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLOMBIA;  
 RX MEDLINE=98290546; PubMed=9628582;  
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.  
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen  
 RT physically assigned P1 and TAC clones.";  
 RL DNA Res. 5:41-54(1998).  
 DR EMBL: AB010070; BAB11446.1; -  
 DR InterPro; IPR003441; NAM.  
 DR Pfam: PF02365; NAM; 1.  
 DR SEQUENCE 329 AA; 37517 MW; 8211824FD93933EC CRC64;  
 SQ SEQUENCE 329 AA; 37517 MW; 8211824FD93933EC CRC64;

Query Match 31.7%; Score 557; DB 10; Length 329;  
 Best Local Similarity 42.2%; Pred. No. 2.4e-45;  
 Matches 127; Conservative 42; Mismatches 78; Indels 54; Gaps

QY 2 ETEEMKESSISWVEAKLPGRFHPKDDLVCDYLMRSLHNHRPPLVLIQVDLNKCE 61  
 Db 10 EDEQMG-----DLPPGFRFHPPTDEELIYHLKHKYLDLGFSAK-AIGVEDLNKAE 58  
 QY 62 PWDIPKMACVGGKDWYFYQSQRDKYATGLRTNRATATGYWKATGKDRITILRKGLVGMKR 121  
 Db 59 PWELPYKAKICEKEWYFFCVRDRKYPTGLRTNRATQAGYWKATGKDRITILRKGLVGMKR 118  
 QY 122 TLVYQGRAPGRKTDWVHFEFLQGS--HHPPNHSLSPPKEDVLCRVFHKNTGEG--- 175  
 Db 119 TLVYQGRAPGRKTDWVHFEFLQGS--HHPPNHSLSPPKEDVLCRVFHKNTGEG--- 174  
 QY 176 -VICRDNMGSCFDEATASLPLMD--PYINFDEPSSYSDHHYIINEHVPCFSNLSQ 232  
 Db 175 PISTLIRIGS---YTGSSLPPLTDSYNDKTKTEPVY-----VPFCSNQAE 219  
 QY 233 NO--TLNSNLTNVSELK-----IPCKNPPLFTGGSSASATLTGLDFSCSSDQWVLR 284  
 Db 220 TRGTILNCFNSPSSLIQDFLQIMPLYPQPSLNISESSNPVLT-----QEQSVLQAM 272  
 QY 285 L 285  
 Db 273 M 273

RESULT 6  
 Q40880 PRELIMINARY; PRT; 327 AA.  
 ID Q40880  
 AC Q40880; Q40894;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE NAM GENE.  
 GN NAM.  
 OS Petunia hybrida (Petunia).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; eusterids I; Solanales; Solanaceae; Petunia.  
 OX NCBI\_TaxID=4102;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=W137, AND W138; TISSUE=LEAF, AND CARPEL;  
 RX MEDLINE=96200768; PubMed=8612269;  
 RA Souer E., van Houwelingen A., Kloos D., Mol J., Koes R.;  
 RT "The no apical meristem gene of Petunia is required for pattern  
 RT formation in embryos and flowers and is expressed at meristem and  
 RT primordia boundaries."  
 RL Cell 85:159-170(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=W138; TISSUE=CARPEL;  
 RA Souer E.J.;  
 RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=W138; TISSUE=CARPEL;  
 RA Souer E.J.;  
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X92204; CAA63101.1; -;  
 DR EMBL; X92205; CAA63102.2; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 327 AA; 36788 MW; 94C428A0176A8B3E CRC64;

Query Match 31.4%; Score 552.5; DB 10; Length 327;  
 Best Local Similarity 42.8%; Pred. No. 6.3e-45;  
 Matches 127; Conservative 42; Mismatches 69; Indels 59; Gaps 12;  
 QY 16 EAKLPGRFHPKDDDELCDYLMRRSLHNNRPPVLVLIQVLDLKNCEPDIPKMACVGGKD 75  
 Db 11 DSNLPPGFRFHPDELIYYLLKVLDSNF--TGRAIAEVDLKNCEPDIPKMACVGGKD 69  
 QY 76 WYFYSQRDRKATGRTNRATATGYWKATGKDRITL--RKGLVGRMRTLVFYQGRAPRG 133  
 Db 70 WYFSLRDRKYPTGLRTNRATAGYWKATGKDRISYSSKTSALVCMKKTLYFYGRAPRG 129  
 QY 134 RKTDDWVHFERLOGSHHPNHSLS-SPKEDWVLCRVFKHNTGEGVTCRDNMG-----SCFD 187  
 Db 130 EKSNNWVHMYRDLGKF--AYHVISRSKDEWVISRVFKSCSTVGTTSNGGKKRLNSSFN 187  
 QY 188 -----ETASASLPLMD--PYINFQEPSSYLSDDHYIINEHVPCFSNL----- 230  
 Db 188 NMVQEVSSPSSVSLPPLLESSPYN--TATSAASK-----KEHVSCFTSTIPSPDPS 239  
 QY 231 -----SQNTLNSLTNSVSELKIPCKN-----PN-----PFTGGSAS 264  
 Db 240 SVFDISSNSLTLSLPAPSFSAILDPSFSSRNVSFPPSLRSLQENLHLPLFSGGTSA 296

RESULT 7  
 Q9FLJ2 ID Q9FLJ2 PRELIMINARY; PRT; 336 AA.  
 AC Q9FLJ2;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE NAM (NO APICAL MERISTEM)-LIKE PROTEIN.  
 GN MFB13.32.  
 OS Arabidopsis thaliana (Mouse-ear cross).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=98290546; PubMed=9628582;  
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.  
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen  
 RT physically assigned pl and TAC clones."  
 RL DNA Res. 5:41-54(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB010073; BAB08499.1; -;  
 DR EMBL; AY054644; AAK96835.1; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 336 AA; 38472 MW; 2595C4FBBDB0680 CRC64;

Query Match 31.2%; Score 548; DB 10; Length 336;  
 Best Local Similarity 37.3%; Pred. No. 1.8e-44;  
 Matches 137; Conservative 53; Mismatches 101; Indels 76; Gaps 14;  
 QY 1 MET-----EEMKESISMVEAKLPGRFHPKDDDELCDYLMRRSLHNNRPPVLVLIQ 54  
 Db 1 METFCGFGKEEQMD-----LPGFRFHPDDELITHLHKVLDTSFSAK-AIGE 50  
 QY 55 VDLNKCPEWDIPKMACVGGKDWYFYSDRDKYATGLRTNRATATGYWKATGKDRITLTKG 114  
 Db 51 VDLNKCPEWLPWMAKGEKWEFFCVDRDKYPTGLRTNRATAGYWKATGKDKIYRGK 110  
 QY 115 KLVGMRKTLVYQGRAPRGKRTDWVHFERLOG---SHPPNHSLSPPKEDWVLCRVFKH 171  
 Db 111 SLVGMRKTLVYGRAPRGKRTDWVHFERLOG---KTAKEWVICRVFK 166  
 QY 172 NTEG-----VICRDNMGSCFDETSASLPLMD--PYINFQEPSSYLSDDHYIINE 222  
 Db 167 SAGGKPIISSLRIGSLGTDENPSL--LPSLTDSSPYNDKTKTEPVY----- 212  
 QY 223 HVPFCSN-LSQO--TUNSNLTNSVSELKIPCKNPNPLFTGGSASATLTGLDSCSSDQM 279  
 Db 213 -VPCFSNQTQNOGTTLNCFFSSPVLNSIQADIFHRIPLYQTSLOVSMNLQSPVLTOEHS 271  
 QY 280 VLRALL-----SOLTKI-----DGSGLGPKESQSVGEGSSSLLTDIG 316  
 Db 272 VLHAMENNRQSLKTMVSVQETGVSTDMTDMTDISSDFEFGKRRDFDQEDPSSSTGPVDL- 330  
 QY 317 IPSTVMN 323  
 Db 331 --EPFVN 335

RESULT 8  
 Q9FK44 ID Q9FK44 PRELIMINARY; PRT; 335 AA.  
 AC Q9FK44;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE NAM (NO APICAL MERISTEM)-LIKE PROTEIN.  
 OS Arabidopsis thaliana (Mouse-ear cross).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;



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Db 61 YFLNLIIFPARARAAGRRRAAARGATEWYFFSLHDKRYATQRTNATRGYWK 120
Qy 103 ATGCKORTILRK-----GKLVGRKTLVYQGRAPGRKTDWYMHFRLOG---S 148
Db 121 ATGKDAIVTRRAAGGAAGVAGGVGMRKTLVYQGRAPGRSKTEWYMHFRVDGHAVA 180
Qy 149 HPPNHLSSP---KEDWVLCRVFKH---NTEGVICRDNMGSCFDETSASLPLP--- 197
Db 181 DHPSSSTSSSNLKLKEDWVLCRVFKSRTANPRPVVSGEAAVLSGSLSPPLPVA 240
Qy 198 ---MDPYIN---FDQEPSSYSLDDHHYIINEHVPCFNSLQNTLSNLSVSELKIPC 251
Db 241 PAVIDGYTGGVYEQDSSAGCHHHHRPPTSAALPFKDLTDPRDLLSNMVQ----- 291
Qy 252 KPNPNLFTGGSASATLTGLDSCSSDQWVLRALLSQLTKIDSLGPKESQSYGEGSS 311
Db 292 -----GGGAAAAAAKSEGF-----HLGWSEESSG-----Y 317
Qy 312 LTDIGIPSTVWN 323
Db 318 VQOSAMASQAWN 329

RESULT 11
Q9SM90 PRELIMINARY; PRT; 331 AA.
AC Q9SM90:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ZWH19.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, INDICA;
RA Hong G., Zhao W.;
RT "Oryza sativa genomic DNA, chromosome 4, clone: b6015.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL117264; CAB55403.1;
DR InterPro; IPR003441; NAM.
DR Pfam; PF02365; NAM; 1.
SQ SEQUENCE 331 AA; 35965 MW; 69B798BD5A2E3E36 CRC64;

Query Match 30.8%; Score 542; DB 10; Length 331;
Best Local Similarity 35.1%; Pred. No. 6.6e-44;
Matches 132; Conservative 41; Mismatches 89; Indels 114; Gaps 12;

Qy 15 VEAKLPPGRFRHPKDELVCYDLMR-----SLHNNHRPPLVLIQVLDNKCPEW 63
Db 1 MEANLPPGRFRHPKDELIVLYLHKLGGGGGGGAGEFYGG-----VAMVDVLDNKCPEW 56
Qy 64 DIP-----KWACVGGKDWYFYQGRDKYATGLTRNAT 98
Db 57 ELPAYELHNLIIFFPARARAAGRRRAAARGATEWYFFSLHDKRYATQRTNATRS 116
Qy 99 GYWKATGKORTILRK-----GKLVGRKTLVYQGRAPGRKTDWYMHFRLOG 147
Db 117 GYWKATGKDAIVTRRAAGGAAGVAGGVGMRKTLVYQGRAPGRSKTEWYMHFRVDG 176
Qy 148 ---SHPPNHLSSP---KEDWVLCRVFKH---NTEGVICRDNMGSCFDETSASLPLP 196
Db 177 HAVADHPSSSTSSSNLKLKEDWVLCRVFKSRTANPRPVVSGEAAVLSGSLSPPLPPP 236
Qy 197 L-----MDPYIN---FDQEPSSYSLDDHHYIINEHVPCFNSLQNTLSNLSVSEL 247
Db 237 LPVAPAVIDGYTGGVYEQDSSAGCHHHHRPPTSAALPFKDLTDPRDLLSNMVQ----- 291
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Qy 248 KIFCKNPNLFTGGSASATLTGLDSCSSDQWVLRALLSQLTKIDSLGPKESQSYGEGS 307
Db 292 -----GGGAAAAAAKSEGF-----HLGWSEESSG--- 316
Qy 308 SESLTDIGIPSTVWN 323
Db 317 ---YVQOSAMASQAWN 329

RESULT 12
Q9S851 PRELIMINARY; PRT; 334 AA.
AC Q9S851:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 38.0 KDA PROTEIN.
GN F14G6.2 OR F15M4.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 1 BAC F14G6 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome I BAC F14G6 genomic sequence.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC015450; AAG51953.1;
DR EMBL; AC012394; AAF16659.1;
DR InterPro; IPR003441; NAM.
DR Pfam; PF02365; NAM; 1.
SQ SEQUENCE 334 AA; 38017 MW; 008EF8F3F3220F07 CRC64;

Query Match 30.5%; Score 536.5; DB 10; Length 334;
Best Local Similarity 38.3%; Pred. No. 2.3e-43;
Matches 123; Conservative 44; Mismatches 67; Indels 87; Gaps 11;

Qy 16 EAKLPPGRFRHPKDELVCYDLMRSLHNNHRPPLVLIQVLDNKCPEWIPKMACVGGKD 75
Db 19 ERGLPPGRFRHPKDELITFTYLSKIFHGG--LSGIHISEVDLNRCEPWLPEMAKMGRE 77
Qy 76 WYFYSQDRKYATGLTRNATATGYWKATGKDTILR--KGKLVGRKTLVYQGRAPRG 133
Db 78 WYFYSLDRKYPTGLTRNATATGYWKATGKDEVFSGGGGLVGMKTLVYFKGRAPRG 137
Qy 134 RKTQWVHFEFLQSGHPPNHLSSPKEDWVLCRVFKHTEGVICRDNMGSCFDETA--- 190
Db 138 LKTQWVHFEFLQSGHPPNHLSSPKEDWVLCRVFKHTEGVICRDNMGSCFDETA--- 189
Qy 191 -----SASLPLMDP-----YINFDQEPSSYSLDDHHYIINEHVPCFNSLSONQT 235
Db 190 NLSLSTTHHHHHEALPLLIIEPSNKTLTNF-----PSLEYDDPH-----QYNNNNNF 235
Qy 236 LNSLTSVSELKIPCKNPNPFLTGGGSASATLTGLDSCSSDQWVLRALLSQLTKI---- 291
Db 236 LHGSSGHNIDELK-----ALINPVVSQLNGIIFPS 265
Qy 292 -----DGLGPKESQS 302
Db 266 GNNNDEDDDFNLGVKTEQS 286
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:52:53 ; Search time 33.36 seconds  
(without alignments)  
1078.774 Million cell updates/sec

Title: US-09-889-926-2  
Perfect score: 1757  
Sequence: 1 MEYEEEMKESISVREAKLP.....EGSSESLITDIPSTVWNC 324

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1757	100.0	324	21 AAG45798 Arabidopsis thalia
2	1561	88.8	287	21 AAG22847 Arabidopsis thalia
3	1391	79.2	257	21 AAG17253 Arabidopsis thalia
4	1391	79.2	257	21 AAG22848 Arabidopsis thalia
5	1112	63.3	206	21 AAG17254 Arabidopsis thalia
6	1112	63.3	206	21 AAG22849 Arabidopsis thalia
7	1112	63.3	206	21 AAG45796 Arabidopsis thalia
8	1112	63.3	206	21 AAG45825 Arabidopsis thalia
9	997	56.7	185	21 AAG17255 Arabidopsis thalia
10	997	56.7	185	21 AAG45797 Arabidopsis thalia
11	997	56.7	185	21 AAG45826 Arabidopsis thalia

12	754	42.9	143	21 AAG45798 Arabidopsis thalia
13	754	42.9	143	21 AAG45827 Arabidopsis thalia
14	557	31.7	329	21 AAG06726 Arabidopsis thalia
15	557	31.7	329	21 AAG46660 Arabidopsis thalia
16	555	31.6	315	21 AAG06727 Arabidopsis thalia
17	555	31.6	315	21 AAG17130 Arabidopsis thalia
18	555	31.6	315	21 AAG46661 Arabidopsis thalia
19	555	31.6	315	21 AAG46673 Arabidopsis thalia
20	555	31.6	337	21 AAG17129 Arabidopsis thalia
21	555	31.6	338	21 AAG46672 Arabidopsis thalia
22	548	31.2	336	21 AAG25574 Arabidopsis thalia
23	548	31.2	336	21 AAG27013 Arabidopsis thalia
24	548	31.2	336	21 AAG46690 Arabidopsis thalia
25	548	31.2	343	21 AAG25573 Arabidopsis thalia
26	545.5	31.0	335	21 AAG47296 Arabidopsis thalia
27	545.5	31.0	335	21 AAG02473 Arabidopsis thalia
28	544.5	31.0	323	21 AAG25575 Arabidopsis thalia
29	544.5	31.0	323	21 AAG27014 Arabidopsis thalia
30	544.5	31.0	323	21 AAG46691 Arabidopsis thalia
31	537	30.6	318	21 AAG21814 Arabidopsis thalia
32	533	30.3	318	21 AAG02527 Arabidopsis thalia
33	532.5	30.3	338	21 AAG53465 Arabidopsis thalia
34	531	30.2	352	21 AAG46921 Arabidopsis thalia
35	527	30.0	256	21 AAG02484 Arabidopsis thalia
36	519	29.5	285	21 AAG13615 Arabidopsis thalia
37	519	29.5	285	21 AAG02512 Arabidopsis thalia
38	517	29.4	352	21 AAG16952 Arabidopsis thalia
39	516	29.4	275	21 AAG13616 Arabidopsis thalia
40	477	27.1	351	20 AAG88296 Wheat geminivirus
41	472	26.9	283	21 AAG47297 Arabidopsis thalia
42	470.5	26.8	324	21 AAG22088 Arabidopsis thalia
43	468.5	26.7	320	21 AAG22089 Arabidopsis thalia
44	465.5	26.5	154	20 AAG88294 Wheat geminivirus
45	464.5	26.4	316	21 AAG22090 Arabidopsis thalia

## ALIGNMENTS

RESULT 1  
AAB15081  
ID AAB15081 standard; Protein; 324 AA.  
XX AC AAB15081;  
XX 19-DEC-2000 (first entry)  
XX DE Arabidopsis NACL protein.  
XX DE Arabidopsis NACL protein.  
XX KW NAC 1; genetically modified; larger.  
XX OS Arabidopsis thaliana.  
XX PN WO200047742-A1.  
XX PD 17-AUG-2000.  
XX PF 11-FEB-1999; 99WO-SG00011.  
XX PR 11-FEB-1999; 99WO-SG00011.  
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.  
XX Xie Q, Chua N;  
XX WPI; 2000-506095/45.  
XX N-PSDB; AAA89936.  
PT Isolated NACL gene sequence from Arabidopsis thaliana is used to produce transgenic plants which are larger than the wild type versions  
PS Claim 2; Page 20-21; 35pp; English.

XX The present sequence is Arabidopsis thaliana NAC1 protein. The NAC1 gene  
 CC belongs to the NAC family of genes which may play a role in patterning  
 CC of the shoot and floral meristem. This gene was isolated from an A.  
 CC thaliana cDNA library expressed in Schizosaccharomyces pombe cells. The  
 CC NAC1 gene may be used for making a genetically altered plant which is  
 CC larger than a wild type version of the plant by overexpressing NAC1. The  
 CC modified plant produces larger leaves, larger roots and more lateral  
 CC roots than the wild type version.

XX  
 SQ Sequence 324 AA;

Query Match 100.0%; Score 1757; DB 21; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-172;  
 Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEEEENKESISSWAEKLPGRFRHPKDDVLYMRSLHNNRPPVLVLIQVDLNC 60  
 DB 1 meteeemkessismveaklppgrfrfhpdkddelvcdylmrslhnnhrpplvlvliqvdlnk 60  
 QY 61 EPWDIPKMACVGKDWYFYSORDKYATGLRTNRATATGYWKATGKDRILRKGKLVGM 120  
 DB 61 epwdipkmacvgkdwfyfsqrkyatglrtnratatgywkatkdrtilrkgklvgmr 120  
 QY 121 KTLVFOGRAPGRKTDVWMEFRLOGSHHPNHSLSPEKDWVLCRVFHKTEGVICRD 180  
 DB 121 ktlvfyggrapgrktdvwmhefrlogshhpnhsllspkdwvlcrvfhkntegvicrd 180  
 QY 181 NMGSCDETASLPLMOPYINFDOEPSYLSDDHHYIINEHVPCFNSLQNQTLNSNL 240  
 DB 181 nmgsctetaslpllmopyinfdepsylsddhhyiinehvpfnslnsqntlnsnl 240  
 QY 241 TNSVSELKIPCKNPPLFTGGASATLTGLDSCSDQMVLRALLSOLFKIDGSLGPKE 300  
 DB 241 tnsvselkipcknpplftggasaatlgtldscsdqmvlrallsqltkidgslgpk 300  
 QY 301 QSYGEGSSESLLDIGIPSTVWNC 324  
 DB 301 qsygegsseslltdigipstvwnc 324

RESULT 2  
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 ID AAG22847 standard; Protein; 287 AA.  
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 AC AAG22847;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 25931.  
 XX  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-0301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825.  
 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123548.  
 PR 23-MAR-1999; 99US-0125786.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
 PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.  
 PR 08-APR-1999; 99US-0128714.

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PR 29-OCT-1999; 99US-0162142.

Query Match 79.2%: Score 1391; DB 21; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.7e-134;
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Db 1 macvvgkdwfyfysqdrkyatglrtnratgywkatgkdrtilrkgklygmrttlvyq 60

QY 128 GRAPGRKTDWVHEFRLOGSHHPNHSLSPPKEDWVLCRVFHKNTGEGVTCRDNMGSCFD 187
Db 61 grapgrktdwvhefrlogshhpnhsalsspkedwvlcrvfhkntegvicrdmngscfd 120

QY 188 ETASASLPPLMDPYINFDOEPSYSLSDHYYIINHVPCFNLSONOTLNSLTNSVSEL 247
Db 121 etasaslpplmdpyinfdoepsyslshhyyiinehvpfcnlsonqlnslncsvsel 180

QY 248 KIPCKNPNPLFTGGASATLTGLDSFSSDOMVLRALLSQTIKIDGSLGPKESQSYGEGS 307
Db 181 kipcknnpplftggasatlgldfsfcssdmvrlrallsqtkidgslgpkessygegs 240

QY 308 SESLLTDIGIPSTVWNC 324
Db 241 seslltdigipstvwnc 257

RESULT 5
AAG17254
ID AAG17254 standard; Protein; 206 AA.
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AC AAG17254;  
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DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18204.  
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KW protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
OS EP1033405-A2.  
PN  
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PD 06-SEP-2000.  
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PF  
XX 25-FEB-2000; 2000EP-0301439.  
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PR 29-OCT-1999; 99US-0162142.

Query Match 63.3%; Score 1112; DB 21; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.2e-106;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 179 RDNWGSCEFDETSASLPPLMDPIYINFDQEPSSYLSDDHHYIINEHVPCFSNLSONQTLS 238
Db 61 rdngscfdeetaslpplmdpyinfdqepssylsddhyyiinehvpfcfsnlsqntlns 120

QY 239 NLTNSVSELKIPCKNPFLTGGSASATLTGLDSDFCSSDQWVLRALLSOLTKIDGSLGPK 298
Db 121 nltnsvselkipcknpfltggsasatltgldsfccsdqwmvrlallsqltkidgslgpk 180

QY 299 ESQSYGEGSSILLTDIGIPSTVWNC 324
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## RESULT 6

AAG22849

ID AAG22849 standard; Protein; 206 AA.

XX AC AAG22849;

XX DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 25933.

XX Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

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Best Local Similarity 100.0%; Pred. No. 6, 2e-106;

Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	239	NLTNSVSELKIPCKNPPLFTGGSASATLTGLDSCSSDQWVLRALLSOLTKIDSLGPK	298
Db	121	nltnsvselkipcknpnplftggsasatltgldsfcssdqmwlrallsqtkidslgpk	180

QY 299 ESQSYGEGSSLLTDIGIPSTVWNC 324  
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RESULT 7  
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XX AC AAG45796;  
XX DT 18-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 57540.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
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hybridisation assay; genetic mapping; gene expression control; promoter;
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DT 18-OCT-2000 (first entry)
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
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XX
PD 06-SEP-2000.
XX
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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XX
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QY 320 TVWNC 324
Db 181 tvwnc 185

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KW Protein identification; signal transduction pathway; metabolic pathway;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Query Match 42.9%; Score 754; DB 21; Length 143;
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QY 242 NSVSELKIPCKNPPLFTGGASATITGLDSFCSSDOMVLRALLSQTIDKIDSLGPKESQ 301
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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Query Match 31.7%; Score 557; DB 21; Length 329;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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XX 06-SEP-2000.
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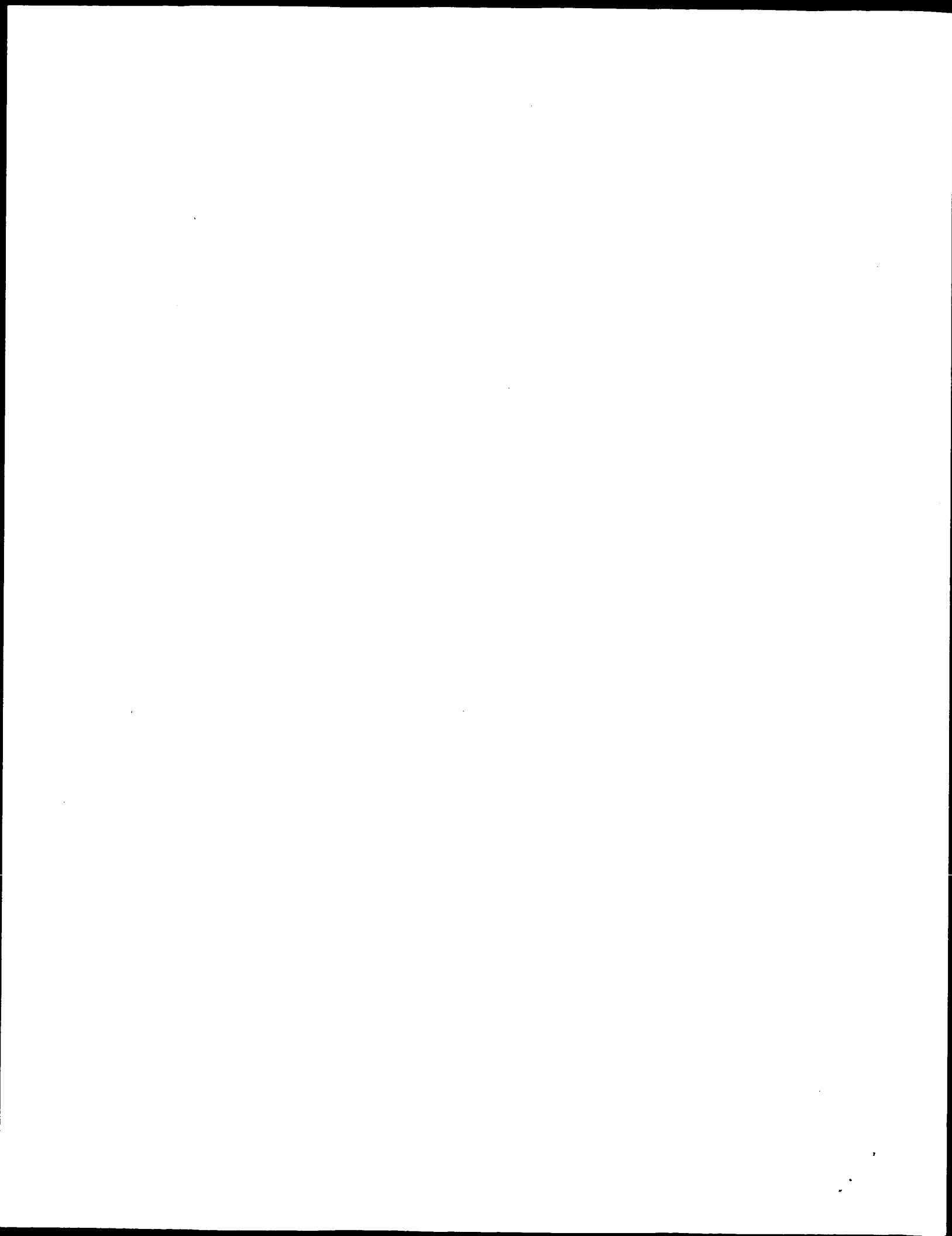
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Query Match 31.7%; Score 557; DB 21; Length 329;
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QY 62 PWDIPKMACVGGKDWYFYQSRDRKYATGLRTNRATATGYKATGKDRFTILRKKLVGMRK 121
Db 59 pwelpykakigekeyffcvdrkyptglrtnratqagywkatgkdeifrgkslvgmkk 118
QY 122 TLVfyQGRAPGRKTDWYHFERLOG---SHHPPNHSLSPPKEDWVLCRVPHKNTGEG--- 175
Db 119 tlvyfyrgrapqgktnwmyheryldgklsahnp-----ktaknewvicrvfhktaggkki 174
QY 176 -VICRDNMGSCFDETASASLPPLMD--PYINFQBPSSYLSDDHHYIINEHVPCFSNLSQ 232
Db 175 pistlirigs---ygtgsslppltdsspyndkkttepy-----vpcfsnqae 219
QY 233 NO--TLNSNLTNSVSELK-----IPCKNPNPLFTGGGSASATLGLDSCSSDQWVLRAL 284
Db 220 trgtlncfnspslssiqpdfqlmiplyqpqslnisessnpvlt-----qedsviqam 272
QY 285 L 285
Db 273 m 273
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Search completed: July 15, 2002, 06:56:42  
Job time: 229 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:54:48 ; Search time 13.14 Seconds  
(without alignments)  
602.275 Million cell updates/sec

Title: US-09-889-926-2  
Perfect score: 1757  
Sequence: 1 METEEMKESISSWEAKLP.....EGSSELLDTGIPSTVWNC 324

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	6.0	1872	1 US-08-188-582-14	Sequence 14, Appl
2	106	6.0	1872	1 US-08-646-715-14	Sequence 14, Appl
3	106	6.0	1893	1 US-08-188-582-11	Sequence 11, Appl
4	106	6.0	1893	1 US-08-646-715-11	Sequence 11, Appl
5	95	5.4	2938	5 PCT-US94-00198-3	Sequence 3, Appl
6	95	5.4	3969	4 US-08-061-376-5	Sequence 5, Appl
7	94	5.4	623	4 US-09-104-068-4	Sequence 4, Appl
8	94	5.4	637	4 US-09-104-068-2	Sequence 2, Appl
9	87.5	5.0	1704	4 US-08-485-355B-40	Sequence 40, Appl
10	84.5	4.8	1182	4 US-09-287-354-6	Sequence 6, Appl
11	81.5	4.6	504	1 US-07-932-915-2	Sequence 2, Appl
12	81.5	4.6	504	5 PCT-US91-05826-2	Sequence 2, Appl
13	81.5	4.6	1207	4 US-09-287-354-5	Sequence 5, Appl
14	81.5	4.6	1481	4 US-09-251-645-14	Sequence 14, Appl
15	80.5	4.6	1863	2 US-08-603-753D-2	Sequence 2, Appl
16	80.5	4.6	1863	4 US-09-099-753-2	Sequence 2, Appl
17	80.5	4.6	1863	4 US-08-986-106-2	Sequence 2, Appl
18	80.5	4.6	1863	4 US-09-007-678B-49	Sequence 49, Appl
19	80	4.6	1142	2 US-08-993-118-7	Sequence 7, Appl
20	80	4.6	1142	3 US-08-845-528C-7	Sequence 7, Appl
21	80	4.6	1142	4 US-09-061-709-2	Sequence 2, Appl
22	79	4.5	427	4 US-08-506-296B-56	Sequence 56, Appl
23	79	4.5	665	4 US-08-506-296B-68	Sequence 68, Appl
24	79	4.5	1253	4 US-08-506-296B-14	Sequence 14, Appl
25	79	4.5	2183	3 US-08-746-111-5	Sequence 5, Appl
26	79	4.5	3898	4 US-08-750-717-2	Sequence 2, Appl
27	79	4.5	4654	4 US-08-476-515A-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1  
US-08-188-582-14  
; Sequence 14; Application US/08188582  
; Patent No. 5534410  
; GENERAL INFORMATION:  
; APPLICANT: Tjian, Robert  
; APPLICANT: Comai, Lucio  
; APPLICANT: Dynlacht, Brian D.  
; APPLICANT: Hoey, Timothy  
; APPLICANT: Ruppert, Siegfried  
; APPLICANT: Tanese, Naoko  
; APPLICANT: Wang, Edith  
; APPLICANT: Weinzierl, Robert O.J.  
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/188,582  
; FILING DATE: 28-JAN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A  
; REGISTRATION NUMBER: 36, 627  
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1872 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-188-582-14

Sequence 84, Appl  
Sequence 86, Appl  
Sequence 88, Appl  
Sequence 90, Appl  
Sequence 8, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 22, Appl  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 24, Appl

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Query Match
Best Local Similarity 6.0%; Score 106; DB 1; Length 1872;
Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

QY 1 METEEMKES--ISMVEAKLP-----GFRHPKDDLVCDYLMR--RSLHNNHRPPL 50
DB 1330 IESADEVRKSLVLPKPKQOLPKKRRVGTTH-----CDYLNRPKHSIHRRTDPM 1382
QY 51 VLIQV-----DLNKEPMDIPKMACVGGKDWYFYSQRDRKYATGLRNRATATGY 100
DB 1383 VTLSSILESINDMRDLPNTPFHTPVNAKV-VKDYKIITRPMDLQT-LREN----- 1433
QY 101 WKATGKRTILRKGVLGMRKTLVYQGRAPGRKTDWVMHEFR-----LQSHHPP 152
DB 1434 -----VKRL--YPSR-----EFRHLELIVKNSATYNGP 1462
QY 153 NHTLSSPKEDWV-LCRVFHNTGVCICRDNMGSCFDEASASLPPLMDPYINFDOEPSSY 211
DB 1463 KHSITQISQMLDLCDEKLKEDKLAR-----LEKAINPLD--DDQVAFSF 1509
QY 212 LSD-----HHYIINEHVPFCFNSLSON-----QTLNSNLT----- 241
DB 1510 ILDNIVTQKMAVPDWPFPVNAKVPDYKYVIVNPMDLTIRKNSKHKYQSRESFL 1569
QY 242 ---NSVSELKIPCKNPPLFTGGSAS-----ATLTGLD-----SFCSSDQWMLRAL 284
DB 1570 DDVNLILANSVKYNGPESQYTKTAQEIYVNCYQTLTEYDEHLETOLEKDICTAKEALEE- 1628
QY 285 LSOLTKID-----GSLGPKESQSYGEGSSSLTLDIGI 317
DB 1629 -AELESDDPMTGPYTPQPPDLYDNTSLMSRDSASV 1664

RESULT 2
US-08-646-715-14
; Sequence 14, Application US/08646715
; Patent No. 5637686
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,715
; FILING DATE: 09-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,582
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
; TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-715-14

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;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/188,582  
;; FILING DATE: 28-JAN-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Osman, Richard A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1893 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-188-582-11

Query Match 6.0%; Score 106; DB 1; Length 1893;  
Best Local Similarity 19.9%; Pred. No. 0.058;  
Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

QY 1 METEEMKSS--ISMVEAKLPP-----GFRFHPKDELVCYDLMR--RSLHNNHRPPL 50  
Db 1351 IESADEVRKSLVLFKPKQQLPPKKRRVGTTH-----CDYLNRPKHSIHRRTDPM 1403  
QY 51 VLIQV-----DLNKCEPMDIPKMACVGGKDWYFYQSQRDKYATGLRTNATATGY 100  
Db 1404 VTLSSILESIIINDRDLPTNTPFHTPVNAKV-VKDYKIIITRPMDLQT-LREN----- 1454  
QY 101 WKATGKDRITLRKGLVGMKRTLVFYQGRAPGRKTDWMHEFR-----LQGSHPHP 152  
Db 1455 -----VRKRL--YPSR-----EPRHLELIVKNSATYNGP 1483  
QY 153 NLSLSPKEDWV-LCRVFHKNTEGVICRDNMGSCFDETSASLPLMDPYINFDQPSY 211  
Db 1484 KHSLTQISQMLDLCDEKLEKEDKLAR-----LEKAINPLD-----DDQVAFSF 1530  
QY 212 LSDD-----HHYIINEHVPCFNSLSON-----QTLNSNLT----- 241  
Db 1531 ILDNIVTQKMAVPDSWPFHPVKNKFPDYKVIIVNPMDETIRKNIKSHKYSRESFL 1590  
QY 242 ---NSVSELKIPCKNPPLTGGAS-----ATLTGLD-----SFCSSDQMVLRAL 284  
Db 1591 DDVNLILANSVKYNGPESQYTKTAQEIIVVVCYQTLTEYDEHLTQLEKDICTAKEAALAE- 1649  
QY 285 LSQTKID----GSLGPKESQSYGEGSSSLLTDIGI 317  
Db 1650 -AELESIDPMTGPTTPQPPDLYDNTSLMSRDSAV 1685

## RESULT 4

US-08-646-715-11  
; Sequence 11, Application US/08646715  
; Patent No. 5637686  
; GENERAL INFORMATION:  
; APPLICANT: Tjian, Robert  
; APPLICANT: Comai, Lucio  
; APPLICANT: Dynlacht, Brian D.  
; APPLICANT: Hoey, Timothy  
; APPLICANT: Ruppert, Siegfried  
; APPLICANT: Tanese, Naoko  
; APPLICANT: Wang, Edith  
; APPLICANT: Weinzierl, Robert O.J.  
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,  
; NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

;; STREET: 4 Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-4187  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/646,715  
;; FILING DATE: 09-MAY-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/188,582  
;; FILING DATE: 28-JAN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Osman, Richard A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1893 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-646-715-11

Query Match 6.0%; Score 106; DB 1; Length 1893;

Best Local Similarity 19.9%; Pred. No. 0.058;  
Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

QY 1 METEEMKSS--ISMVEAKLPP-----GFRFHPKDELVCYDLMR--RSLHNNHRPPL 50  
Db 1351 IESADEVRKSLVLFKPKQQLPPKKRRVGTTH-----CDYLNRPKHSIHRRTDPM 1403  
QY 51 VLIQV-----DLNKCEPMDIPKMACVGGKDWYFYQSQRDKYATGLRTNATATGY 100  
Db 1404 VTLSSILESIIINDRDLPTNTPFHTPVNAKV-VKDYKIIITRPMDLQT-LREN----- 1454  
QY 101 WKATGKDRITLRKGLVGMKRTLVFYQGRAPGRKTDWMHEFR-----LQGSHPHP 152  
Db 1455 -----VRKRL--YPSR-----EPRHLELIVKNSATYNGP 1483  
QY 153 NLSLSPKEDWV-LCRVFHKNTEGVICRDNMGSCFDETSASLPLMDPYINFDQPSY 211  
Db 1484 KHSLTQISQMLDLCDEKLEKEDKLAR-----LEKAINPLD-----DDQVAFSF 1530  
QY 212 LSDD-----HHYIINEHVPCFNSLSON-----QTLNSNLT----- 241  
Db 1531 ILDNIVTQKMAVPDSWPFHPVKNKFPDYKVIIVNPMDETIRKNIKSHKYSRESFL 1590  
QY 242 ---NSVSELKIPCKNPPLTGGAS-----ATLTGLD-----SFCSSDQMVLRAL 284  
Db 1591 DDVNLILANSVKYNGPESQYTKTAQEIIVVVCYQTLTEYDEHLTQLEKDICTAKEAALAE- 1649  
QY 285 LSQTKID----GSLGPKESQSYGEGSSSLLTDIGI 317  
Db 1650 -AELESIDPMTGPTTPQPPDLYDNTSLMSRDSAV 1685

## RESULT 5

PCT-US94-00198-3  
; Sequence 3, Application PC/TUS9400198  
; GENERAL INFORMATION:  
; APPLICANT: Schering Corp.  
; TITLE OF INVENTION: RAS Associated GAP Proteins







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RESULT 12
PCT-US91-05826-2
; Sequence 2, Application PC/TUS9105826
; GENERAL INFORMATION:
;
; APPLICANT: Souillou, Jean-Paul
;
; TITLE OF INVENTION: Protein Polyligands Joined To A Stable Protein
;
; TITLE OF INVENTION: Core
;
; NUMBER OF SEQUENCES: 11
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Bertram I. Rowland, Ph.D. 3400
;
; STREET: 4 Embarcadero Center, Suite 3400
;
; CITY: San Francisco
;
; STATE: California
;
; COUNTRY: USA
;
; ZIP: 94111
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:

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111 LRKGLVGMRKTLVfyOGrapRG--RKTDVWVHEEFRLQSH-----HP----- 151

Db 87 LPPGFLQGPDKTSLVVEGEGRNGERKANWLGSKGLRWEKLAHLAFLAFCGPACPPRYG 146  
QY 152 ---PNHSLSSPKEDWVLCRVFKHNTGVCICRDNMGSCFDETSASLPLMDPYINFDQEP 208  
Db 147 PLIPESSGHKPSDPAFRPLH-----CFLETKILERAPWPTCPPLYL----- 193  
QY 209 SSYLSDDHHYIINEHVPCFNSLSONQTLNSLTVSELKIPCKNPPLFTGGG-----AS 264  
Db 194 -----MSSLPPERSYDPLA-----PSPWVYSGSQPKVPS 223  
QY 265 ATLGLDSECSDDQWVLRALLSQTLLKIDGSL-----GPKESQSYGE--- 305  
Db 224 AFSGSKGFYHKDPNLRPAKEPLAASEGMLGLAPGSHLQQAACDAEGPSLHQDGETGA 283  
QY 306 GSSESLL-TDIGIPSTV 321  
Db 284 GRQCNLCVPFLGYPDV 300

## RESULT 14

US-09-251-645-14  
; Sequence 14, Application US/09251645  
; Patent No. 6281413

## GENERAL INFORMATION:

; APPLICANT: Kramer, Vance C.  
; APPLICANT: Morgan, Michael K.  
; APPLICANT: Anderson, Arne R.  
; APPLICANT: Hart, Hope  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Dunn, Martha  
; APPLICANT: Chen, Jeng S.

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS  
; FILE REFERENCE: CGC1963/A  
; CURRENT APPLICATION NUMBER: US/09/251,645  
; CURRENT FILING DATE: 1999-02-17

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 1481

; TYPE: PRT

; ORGANISM: Photorhabdus luminescens

US-09-251-645-14

Query Match 4.6%; Score 81.5; DB 4; Length 1481;

Best Local Similarity 22.5%; Pred. No. 16;

Matches 78; Conservative 33; Mismatches 90; Indels 145; Gaps 23;

QY 74 KDWYFSQRDRKYATGL-RTNRATATGYWKA-----TG--KDRTLRKGLVGMKRT--- 122  
Db 814 KNW-----YATGIPEVDNTLSAGYWRGDTQAFPTPHFTLWKEGKDVPLTPEDDH 864  
QY 123 LVFYQGRAPRG-----RKTDWMHFRQCSHPPNHSLSPPKEDW---V 164  
Db 865 NLYWLNKALGQPLRSELYGLDGSQAQKIPYVTVESRPQVRQLQDNTILSPVL--WASVV 922  
QY 165 LCRVFHK-----NTEGVCIRDNMGSCFDETSASLP-----PLMDPYINFDQEP--- 208  
Db 923 ERSYHYERIISDPQCNQDITLSSDLFGQPLKQ-VSVQYPRNKKTNPYP--DTLPDTL 979  
QY 209 --SSYLSDD-----HYVINE-----HVP----- 225  
Db 980 FASSY--DQOQQLRLTYOQSWHHLIANELRVGLPDCGTSADFTYDAKHVPVDGLNLE 1037  
QY 226 --CFSN-----LSQNTLNSLTVNSVSELKIPCKNPPLFTGGGSASATLTGLDS 272  
Db 1038 ALCAENSLIADDKPREYLNQRTF-----YTDGKTGDKNPTPLKT-----PTFQALIA 1085  
QY 273 FCSSDQWVLRALLSQ--LTRKIDGSLGPKESQSYGEGSSSELTLTDIG 316  
Db 1086 FTEI-----AVTESLSLSAFDGGTTPDE-----LPGLLTQAG 1117

## RESULT 15

US-08-603-753D-2

; Sequence 2, Application US/08603753D  
; Patent No. 5891857

## GENERAL INFORMATION:

; APPLICANT: HOLT, JEFFREY T.  
; APPLICANT: JENSEN, ROY A.  
; APPLICANT: PAGE, DAVID L.  
; APPLICANT: KING, MARY-CLAIRE  
; APPLICANT: SZABO, CSILLA I.  
; APPLICANT: JETTON, THOMAS L.  
; APPLICANT: ROBINSON-BENION, CHERYL L.  
; APPLICANT: THOMPSON, MARILYN E.

; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2

; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR.

; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER

; CITY: DURHAM

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage

; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1

; SOFTWARE: WORD PERFECT 6.1 and ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/603,753D

; FILING DATE: 20 FEB 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/373,799

; FILING DATE: 17 JAN 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: ARLES A. TAYLOR, JR.

; REGISTRATION NUMBER: 39,395

; REFERENCE/DOCKET NUMBER: 1242/2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919) 493-8000

; TELEFAX: (919) 419-0383

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1863

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: no

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE: adult

; TISSUE TYPE: female breast

; CELL TYPE: ductal carcinoma in situ, invasive

; CELL LINE: breast cancer and normal breast tissue

; ORGANELLE: not derived from a cell line

; IMMEDIATE SOURCE:

; LIBRARY: cDNA library derived from human

; CLONE: obtained using published sequence

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: unknown

; MAP POSITION: unknown

; UNITS: unknown

; FEATURE:



